GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 12, 2005, 22:56:08 ; Search time 164.45 Seconds
(without alignments)
45.484 Million cell updates/sec

Title: US-09-932-322-1
Perfect score: 44
Sequence: 1 XXXCXPXTGCXXX 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	36	81.8	192	2	Q98AR9	Q98ar9 rhizobium l
2	36	81.8	360	2	Q86AK7	Q86ak7 dictyosteli
3	36	81.8	546	2	Q8KJ72	Q8kj72 rhizobium l
4	36	81.8	601	2	Q7M4J3	Q7m4j3 dictyosteli
5	35	79.5	148	2	Q9N018	Q9n018 macaca fasc
6	35	79.5	148	2	Q95KD2	Q95kd2 macaca fasc
7	35	79.5	571	2	Q9AQP5	Q9aqp5 pseudomonas
8	34	77.3	113	2	Q7Z6J7	Q7z6j7 homo sapien
9	34	77.3	145	1	PA2X_NOTSC	P20146 notechis sc
10	34	77.3	167	2	Q7U7V9	Q7u7v9 synechococc
11	34	77.3	312	2	Q9SUV3	Q9suv3 arabidopsis
12	34	77.3	465	2	Q6TVH9	Q6tvh9 bovine papu
13	34	77.3	465	2	AAR98366	Aar98366 bovine pa
14	34	77.3	574	2	Q8LJ36	Q8lj36 oryza sativ
15	34	77.3	998	2	Q869K4	Q869k4 dictyosteli
16	34	77.3	2217	2	Q6Y625	Q6y625 lassa virus
17	34	77.3	2217	2	AAO59515	Aao59515 lassa vir
18	33	75.0	464	2	Q7XV21	Q7xv21 oryza sativ
19	33	75.0	1058	2	Q9LEZ5	Q9lez5 arabidopsis
20	33	75.0	1468	2	Q80TF6	Q80tf6 mus musculu
21	32	72.7	64	2	Q92U25	Q92u25 rhizobium m
22	32	72.7	123	2	Q926M4	Q926m4 listeria in
23	32	72.7	520	2	Q6Z8K1	Q6z8k1 oryza sativ
24	32	72.7	520	2	BAD15642	Bad15642 oryza sat
25	32	72.7	1152	2	Q9FI26	Q9fi26 arabidopsis
26	31	70.5	162	2	Q9WU17	Q9wu17 mesocricetu
27	31	70.5	166	2	Q8T4I5	Q8t4i5 drosophila
28	31	70.5	239	2	Q93KV9	Q93kv9 streptomyce
29	31	70.5	342	2	Q6VMH4	Q6vmh4 streptomyce
30	31	70.5	342	2	AAR30165	Aar30165 streptomy
31	31	70.5	361	2	Q8ECT9	Q8ect9 shewanella
32	31	70.5	482	2	Q9LZR8	Q9lzr8 arabidopsis
33	31	70.5	615	2	Q22886	Q22886 caenorhabdi
34	30	68.2	66	2	Q7N375	Q7n375 photorhabdu
35	30	68.2	78	2	P90569	P90569 plasmodium
36	30	68.2	95	2	P77130	P77130 escherichia
37	30	68.2	100	1	CHA3_BOMMO	P08929 bombyx mori
38	30	68.2	114	2	Q8MQ78	Q8mq78 caenorhabdi
39	30	68.2	119	2	Q8P958	Q8p958 xanthomonas
40	30	68.2	129	1	CHA1_BOMMO	P08826 bombyx mori
41	30	68.2	132	1	CHA2_BOMMO	P08825 bombyx mori
42	30	68.2	133	2	Q9LIW4	Q9liw4 oryza sativ
43	30	68.2	150	2	Q6D216	Q6d216 erwinia car
44	30	68.2	151	2	Q8ZD76	Q8zd76 yersinia pe
45	30	68.2	151	2	AAS62716	Aas62716 yersinia

ALIGNMENTS

RESULT 1
Q98AR9
ID Q98AR9 PRELIMINARY; PRT; 192 AA.
AC Q98AR9;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mlr5880 protein.
GN OrderedLocusNames=mlr5880;
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082936; PubMed=11214974;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti (supplement).";
RL DNA Res. 7:381-406(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003007; BAB52253.1; -.
DR HSSP; Q9ZFY9; 1FK8.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR002347; Adh_short_C2.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00081; GDHRDH.
KW Complete proteome.
SQ SEQUENCE 192 AA; 20183 MW; FD2F660D156037BC CRC64;

Query Match 81.8%; Score 36; DB 2; Length 192;
Best Local Similarity 71.4%; Pred. No. 27;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CXPXTGC 10
| | |||

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Db        176 CSPATGC 182


RESULT 2
Q86AK7
ID   Q86AK7      PRELIMINARY;      PRT;   360 AA.
AC   Q86AK7;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Similar to Dictyostelium discoideum (Slime mold). Prestalk
DE   protein.
OS   Dictyostelium discoideum (Slime mold).
OC   Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX   NCBI_TaxID=44689;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=AX4;
RX   MEDLINE=22092622; PubMed=12097910;
RA   Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA   Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA   Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT   "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RL   Nature 418:79-85(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=AX4;
RA   Baumgart C.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC116984; AAO51380.1; -.
DR   HSSP; P01382; 1NTN.
DR   InterPro; IPR002172; LDL_receptor_A.
DR   InterPro; IPR001673; S_mold_repeat.
DR   Pfam; PF00526; Dicty_CTDC; 13.
DR   PRINTS; PR00261; LDLRECEPTOR.
SQ   SEQUENCE   360 AA;  38013 MW;  4B0061ABA26ED81E CRC64;

  Query Match             81.8%;  Score 36;  DB 2;  Length 360;
  Best Local Similarity   71.4%;  Pred. No. 49;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CXPXTGC 10
              | | |||
Db        211 CSPSTGC 217


RESULT 3
Q8KJ72
ID   Q8KJ72      PRELIMINARY;      PRT;   546 AA.
AC   Q8KJ72;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   PUTATIVE SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE PROTEIN.
GN   Name=msi329;
OS   Rhizobium loti (Mesorhizobium loti).
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Phyllobacteriaceae; Mesorhizobium.
OX   NCBI_TaxID=381;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=R7A;
RX   MEDLINE=21999272; PubMed=12003951;
RA   Sullivan J.T., Trzebiatowski J.R., Cruickshank R.W., Gouzy J.,
RA   Brown S.D., Elliot R.M., Fleetwood D.J., McCallum N.G., Rossbach U.,
RA   Stuart G.S., Weaver J.E., Webby R.J., de Bruijn F.J., Ronson C.W.;
RT   "Comparative sequence analysis of the symbiosis island of
RT   Mesorhizobium loti strain R7A.";
RL   J. Bacteriol. 184:3086-3095(2002).
CC   -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC       (SDR) family.
DR   EMBL; AL672114; CAD31361.1; -.
DR   HSSP; P50163; 2AE1.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0008152; P:metabolism; IEA.
DR   InterPro; IPR002198; ADH_short.
DR   InterPro; IPR002347; Adh_short_C2.
DR   Pfam; PF00106; adh_short; 2.
DR   PRINTS; PR00081; GDHRDH.
DR   PRINTS; PR00080; SDRFAMILY.
DR   PROSITE; PS00061; ADH_SHORT; 1.
KW   Oxidoreductase.
SQ   SEQUENCE   546 AA;  56900 MW;  091D2EFED8E55A9C CRC64;

  Query Match             81.8%;  Score 36;  DB 2;  Length 546;
  Best Local Similarity   71.4%;  Pred. No. 72;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CXPXTGC 10
              | | |||
Db        530 CSPATGC 536


RESULT 4
Q7M4J3
ID   Q7M4J3      PRELIMINARY;      PRT;   601 AA.
AC   Q7M4J3;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   DIF-induced prestalk pDd63 protein precursor (Fragments).
OS   Dictyostelium discoideum (Slime mold).
OC   Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX   NCBI_TaxID=44689;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87187613; PubMed=3568124;
RA   Williams J.G., Ceccarelli A., McRobbie S., Mahbubani H., Kay R.R.,
RA   Early A., Berks M., Jermyn K.A.;
RT   "Direct induction of Dictyostelium prestalk gene expression by DIF
RT   provides evidence that DIF is a morphogen.";
RL   Cell 49:185-192(1987).
DR   PIR; A27020; A27020.
DR   InterPro; IPR001673; S_mold_repeat.
DR   Pfam; PF00526; Dicty_CTDC; 19.
FT   NON_TER     601     601
SQ   SEQUENCE   601 AA;  63359 MW;  7D4433616CDAC438 CRC64;

  Query Match             81.8%;  Score 36;  DB 2;  Length 601;
  Best Local Similarity   71.4%;  Pred. No. 79;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CXPXTGC 10
              | | |||
Db        245 CSPSTGC 251


RESULT 5
Q9N018
ID   Q9N018      PRELIMINARY;      PRT;   148 AA.
AC   Q9N018;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Cerebellum cortex;
RA   Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA   Suzuki Y., Sugano S., Hashimoto K.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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DR   EMBL; AB046629; BAB03547.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   148 AA;  15495 MW;  6242BCE430C6E13B CRC64;

  Query Match             79.5%;  Score 35;  DB 2;  Length 148;
  Best Local Similarity   71.4%;  Pred. No. 33;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CXPXTGC 10
              | | |||
Db         74 CGPSTGC 80


RESULT 6
Q95KD2
ID   Q95KD2      PRELIMINARY;      PRT;   148 AA.
AC   Q95KD2;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Medulla oblogata;
RA   Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA   Suzuki Y., Sugano S., Hashimoto K.;
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB062948; BAB60737.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   148 AA;  15473 MW;  C8D2AA301E0C8191 CRC64;

  Query Match             79.5%;  Score 35;  DB 2;  Length 148;
  Best Local Similarity   71.4%;  Pred. No. 33;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CXPXTGC 10
              | | |||
Db         74 CGPSTGC 80


RESULT 7
Q9AQP5
ID   Q9AQP5      PRELIMINARY;      PRT;   571 AA.
AC   Q9AQP5;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Putative ABC transporter subunit.
GN   Name=ORF31;
OS   Pseudomonas resinovorans.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=53412;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CA10;
RX   MEDLINE=97386424; PubMed=9244273;
RA   Sato S., Ouchiyama N., Kimura T., Nojiri H., Yamane H., Omori T.;
RT   "Cloning of genes involved in carbazole degradation of Pseudomonas sp.
RT   strain CA10: nucleotide sequence of genes and characterization of
RT   meta-cleavage enzymes and hydrolase.";
RL   J. Bacteriol. 179:4841-4849(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CA10;
RX   MEDLINE=97386425; PubMed=9244274;
RA   Sato S., Nam J., Kasuga K., Nojiri H., Yamane H., Omori T.;
RT   "Identification and characterization of genes encoding carbazole 1,9a-
RT   dioxygenase in Pseudomonas sp. strain CA10.";
RL   J. Bacteriol. 179:4850-4858(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CA10;
RX   MEDLINE=21264379; PubMed=11371531;
RA   Nojiri H., Sekiguchi H., Maeda K., Urata M., Nakai S., Yoshida T.,
RA   Habe H., Omori T.;
RT   "Genetic characterization and evolutionary implications of car gene
RT   cluster in carbazole-degrader, Pseudomonas sp. strain CA10.";
RL   J. Bacteriol. 183:3663-3679(2001).
DR   EMBL; AB047548; BAB32742.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR001851; Bac_inmem_transp.
DR   InterPro; IPR001865; Ribosomal_S2.
DR   Pfam; PF02653; BPD_transp_2; 2.
DR   PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
SQ   SEQUENCE   571 AA;  60653 MW;  9A8854777078C186 CRC64;

  Query Match             79.5%;  Score 35;  DB 2;  Length 571;
  Best Local Similarity   71.4%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CXPXTGC 10
              | | |||
Db        565 CGPSTGC 571


RESULT 8
Q7Z6J7
ID   Q7Z6J7      PRELIMINARY;      PRT;   113 AA.
AC   Q7Z6J7;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC053646; AAH53646.1; -.
KW   Hypothetical protein.
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SQ   SEQUENCE   113 AA;  11613 MW;  8624A42297F4A3FF CRC64;

  Query Match             77.3%;  Score 34;  DB 2;  Length 113;
  Best Local Similarity   71.4%;  Pred. No. 40;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CXPXTGC 10
              | | |||
Db        103 CYPKTGC 109


RESULT 9
PA2X_NOTSC
ID   PA2X_NOTSC     STANDARD;      PRT;   145 AA.
AC   P20146;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Probable phospholipase A2 precursor (EC 3.1.1.4) (Phosphatidylcholine
DE   2-acylhydrolase).
OS   Notechis scutatus scutatus (Mainland tiger snake) (Common tiger
OS   snake).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Elapidae; Acanthophiinae; Notechis.
OX   NCBI_TaxID=70142;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RA   Ducancel F.;
RL   Submitted (JAN-1989) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
CC       acyl groups in 3-sn-phosphoglycerides.
CC   -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC       acylglycerophosphocholine + a carboxylate.
CC   -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the phospholipase A2 family. Group I
CC       subfamily.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   ---------------------------------------------------------------------
DR   EMBL; X14043; CAA32201.1; -.
DR   PIR; S07983; S07983.
DR   HSSP; P00608; 1AE7.
DR   InterPro; IPR001211; PhospholipaseA2.
DR   Pfam; PF00068; Phospholip_A2_1; 1.
DR   PRINTS; PR00389; PHPHLIPASEA2.
DR   ProDom; PD000303; PhospholipaseA2; 1.
DR   SMART; SM00085; PA2c; 1.
DR   PROSITE; PS00119; PA2_ASP; 1.
DR   PROSITE; PS00118; PA2_HIS; 1.
KW   Calcium; Hydrolase; Lipid degradation; Multigene family; Signal.
FT   SIGNAL        1     21       Potential.
FT   PROPEP       22     27       Potential.
FT   CHAIN        28    145       Probable phospholipase A2.
FT   ACT_SITE     75     75       By similarity.
FT   ACT_SITE    119    119       By similarity.
FT   DISULFID     38     98       By similarity.
FT   DISULFID     54    144       By similarity.
FT   DISULFID     56     72       By similarity.
FT   DISULFID     71    125       By similarity.
FT   DISULFID     78    118       By similarity.
FT   DISULFID     87    111       By similarity.
FT   DISULFID    105    116       By similarity.
FT   METAL        55     55       Calcium (via carbonyl oxygen) (By
FT                                similarity).
FT   METAL        57     57       Calcium (via carbonyl oxygen) (By
FT                                similarity).
FT   METAL        76     76       Calcium (By similarity).
SQ   SEQUENCE   145 AA;  16002 MW;  38E36029AEE5FAC9 CRC64;

  Query Match             77.3%;  Score 34;  DB 1;  Length 145;
  Best Local Similarity   71.4%;  Pred. No. 50;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CXPXTGC 10
              | | |||
Db        105 CDPETGC 111


RESULT 10
Q7U7V9
ID   Q7U7V9      PRELIMINARY;      PRT;   167 AA.
AC   Q7U7V9;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical precursor.
GN   OrderedLocusNames=SYNW0871;
OS   Synechococcus sp. (strain WH8102).
OC   Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX   NCBI_TaxID=84588;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22825697; PubMed=12917641; DOI=10.1038/nature01943;
RA   Palenik B., Brahamsha B., Larimer F.W., Land M.L., Hauser L.,
RA   Chain P., Lamerdin J.E., Regala W., Allen E.E., McCarren J.,
RA   Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.;
RT   "The genome of a motile marine Synechococcus.";
RL   Nature 424:1037-1042(2003).
DR   EMBL; BX569691; CAE07386.1; -.
KW   Complete proteome; Hypothetical protein; Signal.
FT   SIGNAL        1     22       Potential.
SQ   SEQUENCE   167 AA;  18419 MW;  0B3AFB830ECF971C CRC64;

  Query Match             77.3%;  Score 34;  DB 2;  Length 167;
  Best Local Similarity   71.4%;  Pred. No. 58;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CXPXTGC 10
              | | |||
Db        133 CYPGTGC 139


RESULT 11
Q9SUV3
ID   Q9SUV3      PRELIMINARY;      PRT;   312 AA.
AC   Q9SUV3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein F8B4.80 (Hypothetical protein AT4g32380).
GN   Name=F8B4.80; Synonyms=AT4g32380;
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bevan M., Terryn N., Ardiles W., Buysshaert C., Dasseville R.,
RA   De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,
RA   Villaroel R., Gielen J., Van Montagu M., Hoheisel J., Mewes H.W.,
RA   Mayer K.F.X., Lemcke K., Schueller C.;
RL   Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   EU Arabidopsis sequencing project;
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
```

```
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Terryn N., Ardiles W., Buysshaert C., Dasseville R., De Clerck R.,
RA   De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villaroel R.,
RA   Gielen J., Van Montagu M., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   EU Arabidopsis sequencing project;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to family 28 of glycosyl hydrolases.
DR   EMBL; AL034567; CAA22565.1; -.
DR   EMBL; AL161581; CAB79955.1; -.
DR   PIR; T05348; T05348.
DR   GO; GO:0004650; F:polygalacturonase activity; IEA.
DR   GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR   InterPro; IPR000743; Glyco_hydro_28.
DR   InterPro; IPR006626; PbH1.
DR   InterPro; IPR011050; Pectin_lyas_like.
DR   Pfam; PF00295; Glyco_hydro_28; 2.
DR   SMART; SM00710; PbH1; 3.
KW   Cell wall; Glycosidase; Hydrolase; Hypothetical protein.
SQ   SEQUENCE   312 AA;  34095 MW;  E2E70A2622F30EE0 CRC64;

  Query Match             77.3%;  Score 34;  DB 2;  Length 312;
  Best Local Similarity   71.4%;  Pred. No. 1e+02;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CXPXTGC 10
              | | |||
Db        208 CDPNTGC 214


RESULT 12
Q6TVH9
ID   Q6TVH9      PRELIMINARY;      PRT;   465 AA.
AC   Q6TVH9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Bovine papular stomatitis virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Parapoxvirus.
OX   NCBI_TaxID=129727;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BV-AR02;
RX   PubMed=14671098;
RA   Delhon G., Tulman E.R., Afonso C.L., Lu Z.,
RA   de la Concha-Bermejillo A., Lehmkuhl H.D., Piccone M.E., Kutish G.F.,
RA   Rock D.L.;
RT   "Genomes of the Parapoxviruses Orf Virus and Bovine Papular
RT   Stomtatitis Virus.";
RL   J. Virol. 78:168-177(2004).
DR   EMBL; AY386265; AAR98366.1; -.
DR   InterPro; IPR007027; Pox_F11.
DR   Pfam; PF04943; Pox_F11; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   465 AA;  51404 MW;  BD735469CBED1B79 CRC64;

  Query Match             77.3%;  Score 34;  DB 2;  Length 465;
  Best Local Similarity   71.4%;  Pred. No. 1.5e+02;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CXPXTGC 10
              | | |||
Db         26 CVPRTGC 32


RESULT 13
AAR98366
ID   AAR98366     PRELIMINARY;      PRT;   465 AA.
AC   AAR98366;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Bovine papular stomatitis virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Parapoxvirus.
OX   NCBI_TaxID=129727;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BV-AR02;
RX   PubMed=14671098;
RA   Delhon G., Tulman E.R., Afonso C.L., Lu Z.,
RA   de la Concha-Bermejillo A., Lehmkuhl H.D., Piccone M.E., Kutish G.F.,
RA   Rock D.L.;
RT   "Genomes of the Parapoxviruses Orf Virus and Bovine Papular
RT   Stomtatitis Virus.";
RL   J. Virol. 78:168-177(2004).
DR   EMBL; AY386265; AAR98366.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   465 AA;  51404 MW;  BD735469CBED1B79 CRC64;

  Query Match             77.3%;  Score 34;  DB 2;  Length 465;
  Best Local Similarity   71.4%;  Pred. No. 1.5e+02;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CXPXTGC 10
              | | |||
Db         26 CVPRTGC 32


RESULT 14
Q8LJ36
ID   Q8LJ36      PRELIMINARY;      PRT;   574 AA.
AC   Q8LJ36;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   P0413G02.18 protein.
GN   Name=P0413G02.18;
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA   Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA   Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA   Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA   Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA   Ikeno M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
RA   Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA   Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA   Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA   Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K, Shibata M.,
RA   Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA   Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA   Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA   Yano M., Jiang J., Gojobori T.;
RT   "The genome sequence and structure of rice chromosome 1.";
RL   Nature 420:312-316(2002).
DR   EMBL; AP003344; BAC07361.1; -.
DR   HSSP; P20142; 1AVF.
DR   Gramene; Q8LJ36; -.
DR   GO; GO:0004194; F:pepsin A activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001461; Peptidase_A1.
DR   InterPro; IPR009007; Pept_Aspartic.
DR   Pfam; PF00026; Asp; 1.
DR   PRINTS; PR00792; PEPSIN.
```

```
SQ   SEQUENCE   574 AA;  60980 MW;  A2D654446084F35F CRC64;

  Query Match             77.3%;  Score 34;  DB 2;  Length 574;
  Best Local Similarity   71.4%;  Pred. No. 1.9e+02;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CXPXTGC 10
              | | |||
Db        119 CSPCTGC 125


RESULT 15
Q869K4
ID   Q869K4      PRELIMINARY;      PRT;   998 AA.
AC   Q869K4;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Similar to Mus musculus (Mouse). Tenascin X.
OS   Dictyostelium discoideum (Slime mold).
OC   Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX   NCBI_TaxID=44689;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=AX4;
RX   MEDLINE=22092622; PubMed=12097910;
RA   Gloeckner G.; Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA   Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA   Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT   "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RL   Nature 418:79-85(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=AX4;
RA   Baumgart C.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC115598; AAO53206.1; -.
DR   HSSP; P01132; 1EGF.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR000742; EGF_2.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR006210; IEGF.
DR   InterPro; IPR002049; Laminin_EGF.
DR   Pfam; PF00008; EGF; 7.
DR   PRINTS; PR00011; EGFLAMININ.
DR   SMART; SM00181; EGF; 9.
DR   PROSITE; PS00022; EGF_1; UNKNOWN_10.
DR   PROSITE; PS01186; EGF_2; 7.
DR   PROSITE; PS50026; EGF_3; 6.
SQ   SEQUENCE   998 AA;  106001 MW;  F79BEF394D3E2369 CRC64;

  Query Match             77.3%;  Score 34;  DB 2;  Length 998;
  Best Local Similarity   71.4%;  Pred. No. 3.1e+02;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CXPXTGC 10
              | | |||
Db        609 CNPFTGC 615


Search completed: January 12, 2005, 23:15:11
Job time : 168.45 secs
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N/A

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 12, 2005, 23:04:08 ; Search time 31.2 Seconds
(without alignments)
40.090 Million cell updates/sec

Title: US-09-932-322-1
Perfect score: 44
Sequence: 1 XXXCXPXTGCXXX 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	36	81.8	601	2	A27020	DIF-induced presta
2	34	77.3	145	2	S07983	phospholipase A2 h
3	34	77.3	312	2	T05348	hypothetical prote
4	33	75.0	1058	2	T50496	hypothetical prote
5	32	72.7	64	2	F96006	hypothetical prote
6	31	70.5	482	2	T48397	S-receptor kinase-
7	31	70.5	643	2	T25473	hypothetical prote
8	30	68.2	129	2	A24255	chorion class A pr
9	30	68.2	132	2	B24255	chorion class A pr
10	30	68.2	151	2	AB0331	sigma E factor reg
11	30	68.2	199	2	T49486	hypothetical prote
12	30	68.2	200	2	S04926	wound-induced prot
13	30	68.2	201	2	T07729	wound-induced prot
14	30	68.2	211	2	T04098	CBP20 preproprotei
15	30	68.2	211	2	S04927	wound-induced prot
16	30	68.2	222	1	WMVZB4	antithrombin-III h
17	30	68.2	224	2	E84326	hypothetical prote
18	30	68.2	336	2	A83801	ABC transporter (s
19	30	68.2	345	1	WMVZW2	antithrombin-III h
20	30	68.2	406	2	T23898	hypothetical prote
21	30	68.2	430	2	T23899	hypothetical prote
22	30	68.2	551	2	S01793	arylsulfatase (EC
23	30	68.2	551	2	S07089	arylsulfatase (EC
24	30	68.2	648	2	T23864	hypothetical prote
25	30	68.2	1722	2	E89753	protein F11C7.4 [i
26	29	65.9	46	2	H71262	hypothetical prote
27	29	65.9	119	2	B45937	early chorion prot
28	29	65.9	119	2	S24292	chorion protein -
29	29	65.9	119	2	S24294	chorion protein -
30	29	65.9	119	2	S24291	chorion protein -
31	29	65.9	121	2	S24293	chorion class CA p
32	29	65.9	147	2	E82523	hypothetical prote
33	29	65.9	163	2	T33130	hypothetical prote
34	29	65.9	245	2	F84680	hypothetical prote
35	29	65.9	333	2	F90172	hypothetical prote
36	29	65.9	348	2	T35248	probable oxidoredu
37	29	65.9	375	2	A83636	hypothetical prote
38	29	65.9	379	2	S14885	hypothetical prote
39	29	65.9	449	2	E96676	hypothetical prote
40	29	65.9	507	2	T23375	hypothetical prote
41	29	65.9	513	2	D88991	protein apx-1 [imp
42	29	65.9	685	2	JC7570	Delta-4 protein -
43	29	65.9	686	2	JC7569	Delta-4 protein -
44	29	65.9	753	2	T28787	hypothetical prote
45	29	65.9	843	1	A27340	complement C7 prec

ALIGNMENTS

RESULT 1
A27020
DIF-induced prestalk pDd63 protein precursor - slime mold (Dictyostelium discoideum) (f
C;Species: Dictyostelium discoideum
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: A27020
R;Williams, J.G.; Ceccarelli, A.; McRobbie, S.; Mahbubani, H.; Kay, R.R.; Early, A.; Be
Cell 49, 185-192, 1987
A;Title: Direct induction of Dictyostelium prestalk gene expression by DIF provides evi
A;Reference number: A27020; MUID:87187613; PMID:3568124
A;Accession: A27020
A;Molecule type: DNA
A;Residues: 1-601 <WIL>
A;Cross-references: UNIPROT:Q7M4J3
C;Genetics:
A;Gene: pDd63
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-601/Product: DIF-induced prestalk pDd63 protein #status predicted <MAT>

Query Match 81.8%; Score 36; DB 2; Length 601;
Best Local Similarity 71.4%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          4 CXPXTGC 10
              | | |||
Db        245 CSPSTGC 251
```

RESULT 2
S07983
phospholipase A2 homolog precursor - common tiger snake
C;Species: Notechis scutatus scutatus (common tiger snake, mainland tiger snake)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: S07983
R;Ducancel, F.
submitted to the EMBL Data Library, January 1989
A;Reference number: S07983
A;Accession: S07983
A;Molecule type: mRNA
A;Residues: 1-145 <DUC>
A;Cross-references: UNIPROT:P20146; EMBL:X14043; NID:g64109; PIDN:CAA32201.1; PID:g6411
C;Superfamily: phospholipase A2
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-145/Product: phospholipase A2 #status predicted <MAT>

Query Match 77.3%; Score 34; DB 2; Length 145;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          4 CXPXTGC 10
              | | |||
Db        105 CDPETGC 111
```

RESULT 3
T05348
hypothetical protein F8B4.80 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T05348
R;Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; De
ewes, H.W.; Mayer, K.F.X.; Schueller, C.
submitted to the Protein Sequence Database, February 1999
A;Reference number: Z15409
A;Accession: T05348
A;Molecule type: DNA
A;Residues: 1-312 <BEV>
A;Cross-references: UNIPROT:Q9SUV3; EMBL:AL034567
A;Experimental source: cultivar Columbia; BAC clone F8B4
C;Genetics:
A;Map position: 4
A;Introns: 1/3; 44/3; 101/3; 139/3; 180/3
A;Note: F8B4.80

Query Match 77.3%; Score 34; DB 2; Length 312;
Best Local Similarity 71.4%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CXPXTGC 10
| | |||
Db 208 CDPNTGC 214

RESULT 4
T50496
hypothetical protein T22D6.50 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C;Accession: T50496
R;Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; De
ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25101
A;Accession: T50496
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1058 <BEV>
A;Cross-references: UNIPROT:Q9LEZ5; EMBL:AL357612
A;Experimental source: cultivar Columbia; BAC clone T22D6
C;Genetics:
A;Map position: 5
A;Introns: 60/3; 195/3; 222/3; 448/3; 492/3; 526/3; 555/2; 591/2; 616/3; 662/2; 715/3; 7
A;Note: T22D6.50

Query Match 75.0%; Score 33; DB 2; Length 1058;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CXPXTGC 10
| | |||
Db 1019 CPPETGC 1025

RESULT 5
F96006
hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymB
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: F96006
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernar
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: F96006
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-64 <KUR>
A;Cross-references: UNIPROT:Q92U25; GB:AL591985; PIDN:CAC49718.1; PID:g15141205; GSPDB:
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: SMb21688
A;Genome: plasmid

Query Match 72.7%; Score 32; DB 2; Length 64;
Best Local Similarity 57.1%; Pred. No. 22;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CXPXTGC 10
| | :||
Db 15 CAPSSGC 21

RESULT 6
T48397
S-receptor kinase-like protein - Arabidopsis thaliana
N;Alternate names: protein F17C15.120
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T48397
R;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.
submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24492
A;Accession: T48397
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-482 <BEV>
A;Cross-references: UNIPROT:Q9LZR8; EMBL:AL162506
A;Experimental source: cultivar Columbia; BAC clone F17C15
C;Genetics:
A;Map position: 5
A;Note: F17C15.120

Query Match 70.5%; Score 31; DB 2; Length 482;
Best Local Similarity 57.1%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CXPXTGC 10
| | :||
Db 301 CTPGSGC 307

RESULT 7
T25473
hypothetical protein B0507.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25473
R;Bradshaw, H.
submitted to the EMBL Data Library, July 1996
A;Description: The sequence of C. elegans cosmid B0507.
A;Reference number: Z20039
A;Accession: T25473
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-643 <BRA>
A;Cross-references: UNIPROT:Q22886; EMBL:U64833; PIDN:AAB04822.1; GSPDB:GN00023; CESP:B
A;Experimental source: strain Bristol N2; clone B0507
C;Genetics:
A;Gene: CESP:B0507.1

A;Map position: 5
A;Introns: 59/3; 133/1; 464/3; 586/1

Query Match 70.5%; Score 31; DB 2; Length 643;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          4 CXPXTGC 10
              | | :||
Db        209 CSPQSGC 215
```

RESULT 8
A24255
chorion class A protein L11 precursor - silkworm
C;Species: Bombyx mori (silkworm)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C;Accession: A24255
R;Spoerel, N.; Nguyen, H.T.; Kafatos, F.C.
J. Mol. Biol. 190, 23-35, 1986
A;Title: Gene regulation and evolution in the chorion locus of Bombyx mori. Structural a
A;Reference number: A92929; MUID:87060979; PMID:3023635
A;Accession: A24255
A;Molecule type: DNA
A;Residues: 1-129 <SPO>
A;Cross-references: UNIPROT:P08826; GB:X15557; GB:X04028; GB:X04029; GB:X04030; GB:X0403
C;Superfamily: chorion class A protein pc292
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-129/Product: chorion class A protein L11 #status predicted <MAT>

Query Match 68.2%; Score 30; DB 2; Length 129;
Best Local Similarity 57.1%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          4 CXPXTGC 10
              | |  ||
Db        116 CAPTCGC 122
```

RESULT 9
B24255
chorion class A protein L12 precursor - silkworm
C;Species: Bombyx mori (silkworm)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C;Accession: B24255
R;Spoerel, N.; Nguyen, H.T.; Kafatos, F.C.
J. Mol. Biol. 190, 23-35, 1986
A;Title: Gene regulation and evolution in the chorion locus of Bombyx mori. Structural a
A;Reference number: A92929; MUID:87060979; PMID:3023635
A;Accession: B24255
A;Molecule type: DNA
A;Residues: 1-132 <SPO>
A;Cross-references: UNIPROT:P08825; GB:X15557; GB:X04028; GB:X04029; GB:X04030; GB:X0403
C;Superfamily: chorion class A protein pc292
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-132/Product: chorion class A protein L12 #status predicted <MAT>

Query Match 68.2%; Score 30; DB 2; Length 132;
Best Local Similarity 57.1%; Pred. No. 90;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          4 CXPXTGC 10
              | |  ||
Db        117 CAPTCGC 123
```

RESULT 10
AB0331
sigma E factor regulatory protein rseC [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB0331
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AB0331
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-151 <KUR>
A;Cross-references: UNIPROT:Q8ZD76; GB:AL590842; PIDN:CAC92953.1; PID:g15980692; GSPDB:
C;Genetics:
A;Gene: rseC
C;Superfamily: Escherichia coli sigma-E factor regulatory protein rseC

Query Match 68.2%; Score 30; DB 2; Length 151;
Best Local Similarity 57.1%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          4 CXPXTGC 10
              | | :||
Db         20 CEPHSGC 26
```

RESULT 11
T49486
hypothetical protein B14D6.380 [imported] - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
C;Accession: T49486
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura
submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25022
A;Accession: T49486
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-199 <SCH>
A;Cross-references: EMBL:AL356173; GSPDB:GN00116; NCSP:B14D6.380
A;Experimental source: BAC clone B14D6; strain OR74A
C;Genetics:
A;Gene: NCSP:B14D6.380
A;Map position: 6
C;Superfamily: Neurospora crassa hypothetical protein B14D6.380

Query Match 68.2%; Score 30; DB 2; Length 199;
Best Local Similarity 57.1%; Pred. No. 1.2e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          4 CXPXTGC 10
              | | :||
Db        155 CKPLSGC 161
```

RESULT 12
S04926
wound-induced protein 1 precursor - potato
C;Species: Solanum tuberosum (potato)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: S04926
R;Stanford, A.; Bevan, M.; Northcote, D.
Mol. Gen. Genet. 215, 200-208, 1989
A;Title: Differential expression within a family of novel wound-induced genes in potato
A;Reference number: S04926; MUID:89218921; PMID:2710099
A;Accession: S04926
A;Molecule type: DNA
A;Residues: 1-200 <STA>
A;Cross-references: UNIPROT:P09761; EMBL:X13497; NID:g21617; PIDN:CAA31851.1; PID:g2161
C;Genetics:
A;Gene: win1
A;Introns: 143/3
C;Superfamily: hevein precursor; barwin homology; hevein chitin-binding domain homology
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-200/Product: wound-induced protein 1 #status predicted <MAT>
F;26-69/Domain: hevein chitin-binding domain homology <HCB>

```
F;78-199/Domain: barwin homology <BAR>

  Query Match             68.2%;  Score 30;  DB 2;  Length 200;
  Best Local Similarity   57.1%;  Pred. No. 1.2e+02;
  Matches    4;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 CXPXTGC 10
              | |  ||
Db         56 CSPSQGC 62


RESULT 13
T07729
wound-induced protein (clone TAB7) - tomato (fragment)
C;Species: Lycopersicon esculentum (tomato)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C;Accession: T07729
R;Harris, N.; Taylor, J.E.; Roberts, J.A.
J. Exp. Bot. 48, 1223-1227, 1997
A;Title: Characterization and expression of an mRNA encoding a wound-induced (win) prote
A;Reference number: Z16099
A;Accession: T07729
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-201 <HAR>
A;Cross-references: UNIPROT:O03994; EMBL:U89764; NID:g1888560; PIDN:AAB49688.1; PID:g188
A;Experimental source: strain Ailsa craig; leaf abscission zone tissue
C;Superfamily: hevein precursor; barwin homology; hevein chitin-binding domain homology
F;16-60/Domain: hevein chitin-binding domain homology <HCB>
F;68-188/Domain: barwin homology <BAR>

  Query Match             68.2%;  Score 30;  DB 2;  Length 201;
  Best Local Similarity   57.1%;  Pred. No. 1.2e+02;
  Matches    4;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 CXPXTGC 10
              | |  ||
Db         46 CSPSQGC 52


RESULT 14
T04098
CBP20 preproprotein - common tobacco
N;Alternate names: wound-induced protein
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04098
R;Ponstein, A.S.; Bres-Vloemans, S.A.; Sela-Buurlage, M.B.; Elzen, P.J.; Melchers, L.S.;
Plant Physiol. 104, 109-118, 1994
A;Title: A novel pathogen- and wound-inducible tobacco (Nicotiana tabacum) protein with
A;Reference number: Z15209; MUID:94159785; PMID:8115541
A;Accession: T04098
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-211 <PON>
A;Cross-references: UNIPROT:Q41231; EMBL:S72452; NID:g632733; PIDN:AAB29959.1; PID:g6327
A;Experimental source: cultivar Samsun NN
C;Superfamily: hevein precursor; barwin homology; hevein chitin-binding domain homology
F;23-66/Domain: hevein chitin-binding domain homology <HCB>
F;78-199/Domain: barwin homology <BAR>

  Query Match             68.2%;  Score 30;  DB 2;  Length 211;
  Best Local Similarity   57.1%;  Pred. No. 1.3e+02;
  Matches    4;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 CXPXTGC 10
              | |  ||
Db         53 CSPSQGC 59


RESULT 15
S04927
wound-induced protein 2 precursor - potato
C;Species: Solanum tuberosum (potato)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: S04927
R;Stanford, A.; Bevan, M.; Northcote, D.
Mol. Gen. Genet. 215, 200-208, 1989
A;Title: Differential expression within a family of novel wound-induced genes in potato
A;Reference number: S04926; MUID:89218921; PMID:2710099
A;Accession: S04927
A;Molecule type: DNA
A;Residues: 1-211 <STA>
A;Cross-references: UNIPROT:P09762; EMBL:X13497; NID:g21617; PIDN:CAA31852.1; PID:g2161
C;Genetics:
A;Gene: win2
A;Introns: 142/3
C;Superfamily: hevein precursor; barwin homology; hevein chitin-binding domain homology
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-211/Product: wound-induced protein 2 #status predicted <MAT>
F;26-69/Domain: hevein chitin-binding domain homology <HCB>
F;77-198/Domain: barwin homology <BAR>

  Query Match             68.2%;  Score 30;  DB 2;  Length 211;
  Best Local Similarity   57.1%;  Pred. No. 1.3e+02;
  Matches    4;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 CXPXTGC 10
              | |  ||
Db         56 CSPSQGC 62


Search completed: January 12, 2005, 23:16:03
Job time : 33.2 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 12, 2005, 22:55:47 ; Search time 146.9 Seconds
(without alignments)
31.746 Million cell updates/sec

Title: US-09-932-322-1
Perfect score: 44
Sequence: 1 XXXCXPXTGCXXX 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	35	79.5	79	4	AAU49413	Aau49413 Propionib
2	35	79.5	79	6	ABM45932	Abm45932 Propionib
3	35	79.5	180	7	ABO74428	Abo74428 Pseudomon
4	34	77.3	7	3	AAY62764	Aay62764 PB-cadher
5	34	77.3	7	3	AAY61489	Aay61489 Cadherin-
6	34	77.3	7	3	AAY62007	Aay62007 Cadherin-
7	34	77.3	7	3	AAY62224	Aay62224 Cadherin-
8	34	77.3	7	5	ABJ00550	Abj00550 B lymphoc
9	34	77.3	7	5	ABG33862	Abg33862 B Lymphoc
10	34	77.3	13	5	ABJ00545	Abj00545 B lymphoc
11	34	77.3	13	5	ABG33861	Abg33861 B Lymphoc
12	34	77.3	53	4	AAU44932	Aau44932 Propionib
13	34	77.3	53	6	ABM41451	Abm41451 Propionib
14	34	77.3	113	6	ADA54961	Ada54961 Human pro
15	34	77.3	138	3	AAB42027	Aab42027 Human ORF
16	34	77.3	250	7	ABO75329	Abo75329 Pseudomon
17	34	77.3	312	5	ABB93198	Abb93198 Herbicida
18	34	77.3	540	7	ADF05702	Adf05702 Bacterial
19	34	77.3	3226	4	ABG28408	Abg28408 Novel hum
20	33	75.0	158	4	AAU40006	Aau40006 Propionib
21	33	75.0	158	6	ABM36525	Abm36525 Propionib
22	32	72.7	751	3	AAG43626	Aag43626 Arabidops
23	32	72.7	798	3	AAG43625	Aag43625 Arabidops
24	32	72.7	835	3	AAG43624	Aag43624 Arabidops
25	31	70.5	7	3	AAY63264	Aay63264 Protocadh
26	31	70.5	90	7	ABO81251	Abo81251 Pseudomon
27	31	70.5	114	5	ABP06368	Abp06368 Human ORF
28	31	70.5	148	7	ADJ71040	Adj71040 Human hea
29	31	70.5	183	7	ADF58925	Adf58925 Human pol
30	31	70.5	193	4	AAO00015	Aao00015 Human pol
31	31	70.5	193	7	ADF60298	Adf60298 Human con
32	31	70.5	238	6	ABP99259	Abp99259 Orthosomy
33	31	70.5	239	6	ABP99348	Abp99348 Orthosomy
34	31	70.5	239	6	ABP76713	Abp76713 Streptomy
35	31	70.5	310	7	ABO74638	Abo74638 Pseudomon
36	31	70.5	444	7	ABO70819	Abo70819 Pseudomon
37	31	70.5	482	5	ABB93340	Abb93340 Herbicida
38	31	70.5	580	2	AAW32363	Aaw32363 Mycobacte
39	31	70.5	580	2	AAW32431	Aaw32431 Mycobacte
40	31	70.5	580	2	AAW64303	Aaw64303 Mycobacte
41	31	70.5	580	2	AAW81666	Aaw81666 M. tuberc
42	31	70.5	580	2	AAY38968	Aay38968 M. tuberc
43	31	70.5	580	2	AAY39105	Aay39105 M. tuberc
44	31	70.5	602	2	AAY04996	Aay04996 Mycobacte
45	31	70.5	638	2	AAY04992	Aay04992 Mycobacte

ALIGNMENTS

RESULT 1
AAU49413
ID AAU49413 standard; protein; 79 AA.
XX
AC AAU49413;
XX
DT 13-FEB-2002 (first entry)
XX
DE Propionibacterium acnes immunogenic protein #10309.
XX
KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX
OS Propionibacterium acnes.
XX
PN WO200181581-A2.
XX
PD 01-NOV-2001.
XX
PF 20-APR-2001; 2001WO-US012865.
XX
PR 21-APR-2000; 2000US-0199047P.
PR 02-JUN-2000; 2000US-0208841P.
PR 07-JUL-2000; 2000US-0216747P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
DR WPI; 2001-616774/71.
DR N-PSDB; AAS59545.
XX
PT Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris.
XX
PS Example 1; SEQ ID NO 10608; 1069pp; English.
XX
CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory

CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 79 AA;

Query Match 79.5%; Score 35; DB 4; Length 79;
Best Local Similarity 71.4%; Pred. No. 55;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CXPXTGC 10
| | |||
Db 3 CSPGTGC 9

RESULT 2
ABM45932
ID ABM45932 standard; protein; 79 AA.
XX
AC ABM45932;
XX
DT 20-OCT-2003 (first entry)
XX
DE Propionibacterium acnes predicted ORF-encoded polypeptide #10608.
XX
KW Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
KW immunostimulant; immune response; vaccine.
XX
OS Propionibacterium acnes.
XX
PN WO2003033515-A1.
XX
PD 24-APR-2003.
XX
PF 11-OCT-2002; 2002WO-US032727.
XX
PR 15-OCT-2001; 2001US-00978825.
XX
PA (CORI-) CORIXA CORP.
XX
PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
PI Barth B, Vallieve-Douglass J;
XX
DR WPI; 2003-381789/36.
DR N-PSDB; ACF64474.
XX
PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
PT or for stimulating an immune response specific for a P. acnes protein.
XX
PS Example 1; SEQ ID NO 10608; 1481pp; English.
XX
CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
CC encoding a Propionibacterium acnes protein. The invention also relates to
CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
CC immunogenic fragments of P. acnes polypeptides. The invention
CC additionally encompasses expression vectors and host cells comprising a
CC polynucleotide of the invention; antibodies against polypeptides of the
CC invention; fusion proteins comprising a polypeptide of the invention; a
CC method for stimulating an immune response specific for a P. acnes
CC polypeptide and an isolated T cell population comprising T cells prepared
CC via this method; a vaccine composition (comprising P. acnes polypeptides,
CC polynucleotides, antibodies, fusion proteins, T cell populations, or
CC antigen-presenting cells that express the polypeptide); a method and kit
CC for detecting or determining the presence or absence of P. acnes in a
CC patient; and a method for inhibiting the development of P. acnes in a
CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
CC proteins, T cell populations or antigen-presenting cells that express the
CC polypeptides are useful for diagnosing, preventing or treating acne
CC vulgaris, or for stimulating an immune response specific for a P. acnes
CC protein. The polynucleotides can also be used as probes or primers for
CC nucleic acid hybridisation. The vaccine composition is useful for the
CC stimulation of an immune response against P. acnes, or for treating acne,
CC and the kit is useful for performing a diagnostic assay. The present
CC sequence represents a polypeptide predicted to be encoded by an ORF (open
CC reading frame) contained within the P. acnes polynucleotides of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 79 AA;

Query Match 79.5%; Score 35; DB 6; Length 79;
Best Local Similarity 71.4%; Pred. No. 55;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CXPXTGC 10
| | |||
Db 3 CSPGTGC 9

RESULT 3
ABO74428
ID ABO74428 standard; protein; 180 AA.
XX
AC ABO74428;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polypeptide #6603.
XX
KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI; 2003-615309/58.
DR N-PSDB; ABD07999.
XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 23174; 455pp; English.
XX
CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant

```
CC   production of P. aeruginosa-derived peptides or polypeptides, as target
CC   components for diagnosis and/or treatment of P. aeruginosa-caused
CC   infection, and in detection of P. aeruginosa sequences or other sequences
CC   of Pseudomonas species using biochip technology. Sequences ABO67826-
CC   ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
CC   sequence data for this patent did not form part of the printed
CC   specification but was obtained in electronic format from USPTO at
CC   seqdata.uspto.gov/sequence.html
XX
SQ   Sequence 180 AA;

  Query Match             79.5%;  Score 35;  DB 7;  Length 180;
  Best Local Similarity   71.4%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CXPXTGC 10
              | | |||
Db        124 CRPATGC 130


RESULT 4
AAY62764
ID   AAY62764 standard; peptide; 7 AA.
XX
AC   AAY62764;
XX
DT   02-MAR-2000  (first entry)
XX
DE   PB-cadherin cell adhesion recognition cyclic peptide SEQ ID NO:4047.
XX
KW   Modulation; nonclassical cadherin mediated cell adhesion; CAR;
KW   inhibition; cadherin extracellular domain; cell adhesion recognition;
KW   OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
KW   cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
KW   cadherin related neuronal receptor; LI-cadherin; protocadherin;
KW   desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
KW   rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
KW   neurological disease; cyclic.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Disulfide-bond  1. .7
XX
PN   WO9957149-A2.
XX
PD   11-NOV-1999.
XX
PF   05-MAY-1999;   99WO-CA000363.
XX
PR   05-MAY-1998;   98US-00073040.
PR   06-NOV-1998;   98US-00187859.
PR   20-JAN-1999;   99US-00234395.
PR   08-MAR-1999;   99US-00264516.
XX
PA   (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI   Blaschuk OW,  Gour BJ,  Byers S;
XX
DR   WPI; 2000-038791/03.
XX
PT   New cadherin modulating agents, used for modulating nonclassical cadherin
PT   -mediated functions for treating e.g. cancers, obesity, rheumatoid
PT   arthritis, multiple sclerosis, diabetes or a neurological disease.
XX
PS   Claim 72; Page 193; 252pp; English.
XX
CC   The present invention describes cadherin modulating agents (MA)
CC   comprising peptides which comprise a nonclassical cadherin cell adhesion
CC   recognition (CAR) sequence. The MAs can be used for modulating
CC   nonclassical cadherin-mediated functions. They can be used for e.g.
CC   inhibiting adhesion of nonclassical-cadherin expressing cells in a
CC   mammal, enhancing delivery of a drug through the skin of a mammal,
CC   enhancing delivery of a drug to a tumour in a mammal, treating cancer in
CC   a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
CC   angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
CC   expressing cell, preventing or treating obesity in a mammal, stimulating
CC   blood vessel regression in a mammal, enhancing drug delivery to the
CC   central nervous system, treating a demyelinating neurological disease,
CC   increasing vasopermeability in a mammal, enhancing adhesion of
CC   nonclassical cadherin-expressing cells, inhibiting synaptic stability in
CC   a mammal, or preventing pregnancy in a mammal. They can also be used for
CC   e.g. enhancing or directing neurite outgrowth, facilitating wound healing
CC   or reducing scar tissue, or enhancing adhesion of foreign tissue in a
CC   mammal. They can also be used for treating e.g. psoriasis, arthritis, age
CC   -related macular degeneration, multiple sclerosis and diabetes. The
CC   products can also be used for detection and diagnosis and in bioreactors.
CC   AAY60592 to AAY64572 represent specifically claimed peptides, and
CC   AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in
CC   the exemplification of the present invention
XX
SQ   Sequence 7 AA;

  Query Match             77.3%;  Score 34;  DB 3;  Length 7;
  Best Local Similarity   71.4%;  Pred. No. 1.7e+06;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CXPXTGC 10
              | | |||
Db          1 CDPKTGC 7


RESULT 5
AAY61489
ID   AAY61489 standard; peptide; 7 AA.
XX
AC   AAY61489;
XX
DT   02-MAR-2000  (first entry)
XX
DE   Cadherin-7 cell adhesion recognition cyclic peptide SEQ ID NO:1375.
XX
KW   Modulation; nonclassical cadherin mediated cell adhesion; CAR;
KW   inhibition; cadherin extracellular domain; cell adhesion recognition;
KW   OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
KW   cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
KW   cadherin related neuronal receptor; LI-cadherin; protocadherin;
KW   desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
KW   rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
KW   neurological disease; cyclic.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Disulfide-bond  1. .7
XX
PN   WO9957149-A2.
XX
PD   11-NOV-1999.
XX
PF   05-MAY-1999;   99WO-CA000363.
XX
PR   05-MAY-1998;   98US-00073040.
PR   06-NOV-1998;   98US-00187859.
PR   20-JAN-1999;   99US-00234395.
PR   08-MAR-1999;   99US-00264516.
XX
PA   (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI   Blaschuk OW,  Gour BJ,  Byers S;
XX
DR   WPI; 2000-038791/03.
XX
PT   New cadherin modulating agents, used for modulating nonclassical cadherin
```

PT -mediated functions for treating e.g. cancers, obesity, rheumatoid
PT arthritis, multiple sclerosis, diabetes or a neurological disease.
XX
PS Claim 36; Page 172; 252pp; English.
XX
CC The present invention describes cadherin modulating agents (MA)
CC comprising peptides which comprise a nonclassical cadherin cell adhesion
CC recognition (CAR) sequence. The MAs can be used for modulating
CC nonclassical cadherin-mediated functions. They can be used for e.g.
CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
CC mammal, enhancing delivery of a drug through the skin of a mammal,
CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
CC expressing cell, preventing or treating obesity in a mammal, stimulating
CC blood vessel regression in a mammal, enhancing drug delivery to the
CC central nervous system, treating a demyelinating neurological disease,
CC increasing vasopermeability in a mammal, enhancing adhesion of
CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
CC a mammal, or preventing pregnancy in a mammal. They can also be used for
CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
CC -related macular degeneration, multiple sclerosis and diabetes. The
CC products can also be used for detection and diagnosis and in bioreactors.
CC AAY60592 to AAY64572 represent specifically claimed peptides, and
CC AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in
CC the exemplification of the present invention
XX
SQ Sequence 7 AA;

Query Match 77.3%; Score 34; DB 3; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CXPXTGC 10
| | |||
Db 1 CEPKTGC 7

RESULT 6
AAY62007
ID AAY62007 standard; peptide; 7 AA.
XX
AC AAY62007;
XX
DT 02-MAR-2000 (first entry)
XX
DE Cadherin-12 cell adhesion recognition cyclic peptide SEQ ID NO:1799.
XX
KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;
KW inhibition; cadherin extracellular domain; cell adhesion recognition;
KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
KW neurological disease; cyclic.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1. .7
XX
PN WO9957149-A2.
XX
PD 11-NOV-1999.
XX
PF 05-MAY-1999; 99WO-CA000363.
XX
PR 05-MAY-1998; 98US-00073040.
PR 06-NOV-1998; 98US-00187859.
PR 20-JAN-1999; 99US-00234395.
PR 08-MAR-1999; 99US-00264516.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuk OW, Gour BJ, Byers S;
XX
DR WPI; 2000-038791/03.
XX
PT New cadherin modulating agents, used for modulating nonclassical cadherin
PT -mediated functions for treating e.g. cancers, obesity, rheumatoid
PT arthritis, multiple sclerosis, diabetes or a neurological disease.
XX
PS Claim 48; Page 180; 252pp; English.
XX
CC The present invention describes cadherin modulating agents (MA)
CC comprising peptides which comprise a nonclassical cadherin cell adhesion
CC recognition (CAR) sequence. The MAs can be used for modulating
CC nonclassical cadherin-mediated functions. They can be used for e.g.
CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
CC mammal, enhancing delivery of a drug through the skin of a mammal,
CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
CC expressing cell, preventing or treating obesity in a mammal, stimulating
CC blood vessel regression in a mammal, enhancing drug delivery to the
CC central nervous system, treating a demyelinating neurological disease,
CC increasing vasopermeability in a mammal, enhancing adhesion of
CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
CC a mammal, or preventing pregnancy in a mammal. They can also be used for
CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
CC -related macular degeneration, multiple sclerosis and diabetes. The
CC products can also be used for detection and diagnosis and in bioreactors.
CC AAY60592 to AAY64572 represent specifically claimed peptides, and
CC AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in
CC the exemplification of the present invention
XX
SQ Sequence 7 AA;

Query Match 77.3%; Score 34; DB 3; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CXPXTGC 10
| | |||
Db 1 CDPKTGC 7

RESULT 7
AAY62224
ID AAY62224 standard; peptide; 7 AA.
XX
AC AAY62224;
XX
DT 02-MAR-2000 (first entry)
XX
DE Cadherin-14 cell adhesion recognition cyclic peptide SEQ ID NO:3971.
XX
KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;
KW inhibition; cadherin extracellular domain; cell adhesion recognition;
KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
KW neurological disease; cyclic.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers

```
FT   Disulfide-bond  1. .7
XX
PN   WO9957149-A2.
XX
PD   11-NOV-1999.
XX
PF   05-MAY-1999;   99WO-CA000363.
XX
PR   05-MAY-1998;   98US-00073040.
PR   06-NOV-1998;   98US-00187859.
PR   20-JAN-1999;   99US-00234395.
PR   08-MAR-1999;   99US-00264516.
XX
PA   (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI   Blaschuk OW,  Gour BJ,  Byers S;
XX
DR   WPI; 2000-038791/03.
XX
PT   New cadherin modulating agents, used for modulating nonclassical cadherin
PT   -mediated functions for treating e.g. cancers, obesity, rheumatoid
PT   arthritis, multiple sclerosis, diabetes or a neurological disease.
XX
PS   Claim 54; Page 184; 252pp; English.
XX
CC   The present invention describes cadherin modulating agents (MA)
CC   comprising peptides which comprise a nonclassical cadherin cell adhesion
CC   recognition (CAR) sequence. The MAs can be used for modulating
CC   nonclassical cadherin-mediated functions. They can be used for e.g.
CC   inhibiting adhesion of nonclassical-cadherin expressing cells in a
CC   mammal, enhancing delivery of a drug through the skin of a mammal,
CC   enhancing delivery of a drug to a tumour in a mammal, treating cancer in
CC   a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
CC   angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
CC   expressing cell, preventing or treating obesity in a mammal, stimulating
CC   blood vessel regression in a mammal, enhancing drug delivery to the
CC   central nervous system, treating a demyelinating neurological disease,
CC   increasing vasopermeability in a mammal, enhancing adhesion of
CC   nonclassical cadherin-expressing cells, inhibiting synaptic stability in
CC   a mammal, or preventing pregnancy in a mammal. They can also be used for
CC   e.g. enhancing or directing neurite outgrowth, facilitating wound healing
CC   or reducing scar tissue, or enhancing adhesion of foreign tissue in a
CC   mammal. They can also be used for treating e.g. psoriasis, arthritis, age
CC   -related macular degeneration, multiple sclerosis and diabetes. The
CC   products can also be used for detection and diagnosis and in bioreactors.
CC   AAY60592 to AAY64572 represent specifically claimed peptides, and
CC   AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in
CC   the exemplification of the present invention
XX
SQ   Sequence 7 AA;

  Query Match             77.3%;  Score 34;  DB 3;  Length 7;
  Best Local Similarity   71.4%;  Pred. No. 1.7e+06;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CXPXTGC 10
              | | |||
Db          1 CDPKTGC 7


RESULT 8
ABJ00550
ID   ABJ00550 standard; peptide; 7 AA.
XX
AC   ABJ00550;
XX
DT   05-SEP-2002  (first entry)
XX
DE   B lymphocyte stimulator protein binding peptide #1.
XX
KW   B lymphocyte stimulator protein binding protein; BLyS; immune disease;
KW   allergy; proliferative disease; infectious disease; arteriosclerosis;
KW   inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW   ischaemia; graft-versus-host disease; neurodegenerative disease;
KW   immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW   neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW   antiasthmatic; antiallergic; thyromimetic; antianaemic; haemostatic;
KW   dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW   antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 2
FT                   /label= Phe, Trp, Tyr
FT   Misc-difference 4
FT                   /label= Pro, Tyr
XX
PN   WO200216411-A2.
XX
PD   28-FEB-2002.
XX
PF   17-AUG-2001; 2001WO-US025850.
XX
PR   18-AUG-2000; 2000US-0226700P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Beltzer JP,  Potter DM,  Fleming TL,  Rosen CA;
XX
DR   WPI; 2002-499775/53.
XX
PT   The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT   administering B Lymphocyte stimulator binding polypeptide.
XX
PS   Claim 69; Page 233; 387pp; English.
XX
CC   The present invention relates to the treatment, prevention or
CC   amelioration of a disease or disorder associated with: aberrant B
CC   lymphocyte stimulator (BLyS), BLyS receptor expression or activity; cells
CC   of haematopoietic origin; or proliferative disease; and reducing,
CC   inhibiting or stimulating immunoglobulin production, B cell proliferation
CC   and graft rejection involving administration of BLyS binding polypeptide.
CC   The BLyS binding polypeptides are used in the treatment, prevention or
CC   amelioration of diseases such as immune system diseases, proliferative
CC   diseases, diseases of cells of hematopoietic origin, graft rejection,
CC   allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC   hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC   neurodegenerative diseases. The present sequence is a B lymphocyte
CC   stimulator protein binding peptide
XX
SQ   Sequence 7 AA;

  Query Match             77.3%;  Score 34;  DB 5;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CXPXTGC 10
              |||||||
Db          1 CXPXTGC 7


RESULT 9
ABG33862
ID   ABG33862 standard; peptide; 7 AA.
XX
AC   ABG33862;
XX
DT   15-JUL-2002  (first entry)
XX
DE   B Lymphocyte Stimulator (BLyS) binding peptide #436.
XX
KW   B Lymphocyte Stimulator protein; B Lymphocyte Stimulator binding peptide;
KW   BLyS; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid;
KW   synovial fluid; saliva; mucus.
XX
```

```
OS   Synthetic.
XX
PN   WO200216412-A2.
XX
PD   28-FEB-2002.
XX
PF   17-AUG-2001; 2001WO-US025891.
XX
PR   18-AUG-2000; 2000US-0226489P.
XX
PA   (DYAX-) DYAX CORP.
XX
PI   Beltzer JP,  Potter MD,  Fleming TJ,  Ladner RC;
XX
DR   WPI; 2002-351647/38.
XX
PT   New B-lymphocyte stimulator binding polypeptide useful in detecting or
PT   isolating BLyS or BLyS-like polypeptide comprises a specified amino acid
PT   sequence.
XX
PS   Disclosure; Page 132; 269pp; English.
XX
CC   The invention relates to a B Lymphocyte Stimulator (BLyS) binding
CC   polypeptide. BLyS binding peptides bind BLyS or BLyS-like proteins
CC   reversibly or irreversibly. The binding peptides are used in detection,
CC   isolation and/or purification of BLyS in a solution such as water or a
CC   buffer solution, as well as any fluid and/or cell obtained from an
CC   individual biological fluid, body tissue, body cell, cell line, tissue
CC   culture or other source containing BLyS or BLyS-like polypeptides. The
CC   biological fluids include sera, plasma, lymph, blood, blood fraction,
CC   urine, synovial fluid, spinal fluid, saliva and mucous. Sequences
CC   ABG33406-33415, ABG33423-33575, ABG33588-33846, ABG33848-33850 and
CC   ABG33852-33862 represent BLyS binding peptides of the invention
XX
SQ   Sequence 7 AA;

  Query Match             77.3%;  Score 34;  DB 5;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CXPXTGC 10
              |||||||
Db          1 CXPXTGC 7


RESULT 10
ABJ00545
ID   ABJ00545 standard; peptide; 13 AA.
XX
AC   ABJ00545;
XX
DT   05-SEP-2002  (first entry)
XX
DE   B lymphocyte stimulator protein binding protein consensus peptide #1.
XX
KW   B lymphocyte stimulator protein binding protein; BLyS; immune disease;
KW   allergy; proliferative disease; infectious disease; arteriosclerosis;
KW   inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW   ischaemia; graft-versus-host disease; neurodegenerative disease;
KW   immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW   neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW   antiasthmatic; antiallergic; thyromimetic; antianaemic; haemostatic;
KW   dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW   antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /label= Ala, Asn, Lys, Ser
FT   Misc-difference 2
FT                   /label= Ala, Glu, Met, Ser, Val
FT   Misc-difference 3
FT                   /label= Ala, Asn, Lys, Pro
FT   Misc-difference 5
FT                   /label= Phe, Trp, Tyr
FT   Misc-difference 7
FT                   /label= Pro, Tyr
FT   Misc-difference 11
FT                   /label= Ala, Gln, His, Phe, Val
FT   Misc-difference 12
FT                   /label= Asn, Gln, Gly, His, Ser, Val
FT   Misc-difference 13
FT                   /label= Ala, Asn, Gly, Ile, Pro, Ser
XX
PN   WO200216411-A2.
XX
PD   28-FEB-2002.
XX
PF   17-AUG-2001; 2001WO-US025850.
XX
PR   18-AUG-2000; 2000US-0226700P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Beltzer JP,  Potter DM,  Fleming TL,  Rosen CA;
XX
DR   WPI; 2002-499775/53.
XX
PT   The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT   administering B Lymphocyte stimulator binding polypeptide.
XX
PS   Claim 69; Page 230; 387pp; English.
XX
CC   The present invention relates to the treatment, prevention or
CC   amelioration of a disease or disorder associated with: aberrant B
CC   lymphocyte stimulator (BLyS), BLyS receptor expression or activity; cells
CC   of haematopoietic origin; or proliferative disease; and reducing,
CC   inhibiting or stimulating immunoglobulin production, B cell proliferation
CC   and graft rejection involving administration of BLyS binding polypeptide.
CC   The BLyS binding polypeptides are used in the treatment, prevention or
CC   amelioration of diseases such as immune system diseases, proliferative
CC   diseases, diseases of cells of hematopoietic origin, graft rejection,
CC   allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC   hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC   neurodegenerative diseases. The present sequence is a conserved region of
CC   a B lymphocyte stimulator protein binding peptide
XX
SQ   Sequence 13 AA;

  Query Match             77.3%;  Score 34;  DB 5;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CXPXTGC 10
              |||||||
Db          4 CXPXTGC 10


RESULT 11
ABG33861
ID   ABG33861 standard; peptide; 13 AA.
XX
AC   ABG33861;
XX
DT   15-JUL-2002  (first entry)
XX
DE   B Lymphocyte Stimulator (BLyS) binding peptide #435.
XX
KW   B Lymphocyte Stimulator protein; B Lymphocyte Stimulator binding peptide;
KW   BLyS; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid;
KW   synovial fluid; saliva; mucus.
XX
OS   Synthetic.
XX
PN   WO200216412-A2.
```

XX
PD 28-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-US025891.
XX
PR 18-AUG-2000; 2000US-0226489P.
XX
PA (DYAX-) DYAX CORP.
XX
PI Beltzer JP, Potter MD, Fleming TJ, Ladner RC;
XX
DR WPI; 2002-351647/38.
XX
PT New B-lymphocyte stimulator binding polypeptide useful in detecting or
PT isolating BLyS or BLyS-like polypeptide comprises a specified amino acid
PT sequence.
XX
PS Disclosure; Page 121; 269pp; English.
XX
CC The invention relates to a B Lymphocyte Stimulator (BLyS) binding
CC polypeptide. BLyS binding peptides bind BLyS or BLyS-like proteins
CC reversibly or irreversibly. The binding peptides are used in detection,
CC isolation and/or purification of BLyS in a solution such as water or a
CC buffer solution, as well as any fluid and/or cell obtained from an
CC individual biological fluid, body tissue, body cell, cell line, tissue
CC culture or other source containing BLyS or BLyS-like polypeptides. The
CC biological fluids include sera, plasma, lymph, blood, blood fraction,
CC urine, synovial fluid, spinal fluid, saliva and mucous. Sequences
CC ABG33406-33415, ABG33423-33575, ABG33588-33846, ABG33848-33850 and
CC ABG33852-33862 represent BLyS binding peptides of the invention
XX
SQ Sequence 13 AA;

Query Match 77.3%; Score 34; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CXPXTGC 10
||||||
Db 4 CXPXTGC 10

RESULT 12
AAU44932
ID AAU44932 standard; protein; 53 AA.
XX
AC AAU44932;
XX
DT 27-FEB-2002 (first entry)
XX
DE Propionibacterium acnes immunogenic protein #5828.
XX
KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX
OS Propionibacterium acnes.
XX
PN WO200181581-A2.
XX
PD 01-NOV-2001.
XX
PF 20-APR-2001; 2001WO-US012865.
XX
PR 21-APR-2000; 2000US-0199047P.
PR 02-JUN-2000; 2000US-0208841P.
PR 07-JUL-2000; 2000US-0216747P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
DR WPI; 2001-616774/71.
DR N-PSDB; AAS59524.
XX
PT Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris.
XX
PS Example 1; SEQ ID NO 6127; 1069pp; English.
XX
CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorben assay (ELISA). Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 53 AA;

Query Match 77.3%; Score 34; DB 4; Length 53;
Best Local Similarity 71.4%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CXPXTGC 10
| | |||
Db 33 CRPRTGC 39

RESULT 13
ABM41451
ID ABM41451 standard; protein; 53 AA.
XX
AC ABM41451;
XX
DT 20-OCT-2003 (first entry)
XX
DE Propionibacterium acnes predicted ORF-encoded polypeptide #6127.
XX
KW Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
KW immunostimulant; immune response; vaccine.
XX
OS Propionibacterium acnes.
XX
PN WO2003033515-A1.
XX
PD 24-APR-2003.
XX
PF 11-OCT-2002; 2002WO-US032727.
XX
PR 15-OCT-2001; 2001US-00978825.
XX
PA (CORI-) CORIXA CORP.
XX
PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
PI Barth B, Vallieve-Douglass J;
XX
DR WPI; 2003-381789/36.
DR N-PSDB; ACF64453.

XX
PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
PT or for stimulating an immune response specific for a P. acnes protein.
XX
PS Example 1; SEQ ID NO 6127; 1481pp; English.
XX
CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
CC encoding a Propionibacterium acnes protein. The invention also relates to
CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
CC immunogenic fragments of P. acnes polypeptides. The invention
CC additionally encompasses expression vectors and host cells comprising a
CC polynucleotide of the invention; antibodies against polypeptides of the
CC invention; fusion proteins comprising a polypeptide of the invention; a
CC method for stimulating an immune response specific for a P. acnes
CC polypeptide and an isolated T cell population comprising T cells prepared
CC via this method; a vaccine composition (comprising P. acnes polypeptides,
CC polynucleotides, antibodies, fusion proteins, T cell populations, or
CC antigen-presenting cells that express the polypeptide); a method and kit
CC for detecting or determining the presence or absence of P. acnes in a
CC patient; and a method for inhibiting the development of P. acnes in a
CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
CC proteins, T cell populations or antigen-presenting cells that express the
CC polypeptides are useful for diagnosing, preventing or treating acne
CC vulgaris, or for stimulating an immune response specific for a P. acnes
CC protein. The polynucleotides can also be used as probes or primers for
CC nucleic acid hybridisation. The vaccine composition is useful for the
CC stimulation of an immune response against P. acnes, or for treating acne,
CC and the kit is useful for performing a diagnostic assay. The present
CC sequence represents a polypeptide predicted to be encoded by an ORF (open
CC reading frame) contained within the P. acnes polynucleotides of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 53 AA;

Query Match 77.3%; Score 34; DB 6; Length 53;
Best Local Similarity 71.4%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CXPXTGC 10
| | |||
Db 33 CRPRTGC 39

RESULT 14
ADA54961
ID ADA54961 standard; protein; 113 AA.
XX
AC ADA54961;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human protein, SEQ ID 2529.
XX
KW Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
KW Gene Therapy; human; secretory protein; membrane proteins; cancer;
KW inflammatory disease; osteoporosis; neurological disease.
XX
OS Homo sapiens.
XX
PN EP1293569-A2.
XX
PD 19-MAR-2003.
XX
PF 21-MAR-2002; 2002EP-00006586.
XX
PR 14-SEP-2001; 2001JP-00328381.
PR 24-JAN-2002; 2002US-0350435P.
XX
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI; 2003-395539/38.
DR N-PSDB; ADA53322.
XX
PT New polynucleotides encoding full-length polypeptides, e.g. secretory
PT and/or membrane proteins, useful for developing medicines for diseases in
PT which the gene is involved, or as target molecules for gene therapy.
XX
PS Claim 14; SEQ ID NO 2529; 205pp; English.
XX
CC The present invention relates to novel human secretory or membrane
CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
CC ADA54071). The coding sequences are useful in the gene therapy of
CC diseases caused by abnormalities of the proteins, e.g. cancer,
CC inflammatory diseases, osteoporosis or neurological disease.
XX
SQ Sequence 113 AA;

Query Match 77.3%; Score 34; DB 6; Length 113;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CXPXTGC 10
| | |||
Db 103 CYPKTGC 109

RESULT 15
AAB42027
ID AAB42027 standard; protein; 138 AA.
XX
AC AAB42027;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human ORFX ORF1791 polypeptide sequence SEQ ID NO:3582.
XX
KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cholesterol ester storage; systemic lupus erythematosus; infection;
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW thrombosis; contraceptive.
XX
OS Homo sapiens.
XX
PN WO200058473-A2.
XX
PD 05-OCT-2000.
XX
PF 31-MAR-2000; 2000WO-US008621.
XX
PR 31-MAR-1999; 99US-0127607P.
PR 02-APR-1999; 99US-0127636P.
PR 05-APR-1999; 99US-0127728P.
PR 30-MAR-2000; 2000US-00540763.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX

DR WPI; 2000-602362/57.
DR N-PSDB; AAC76236.
XX
PT Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease.
XX
PS Claim 11; Page 2743; 5507pp; English.
XX
CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC sequences have activities such as: cytostatic; hepatotropic; vulnerary;
CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
CC anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
CC dermatological; immunosuppressive; antiinflammatory; antibacterial;
CC antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The
CC sequences can be used for determining the presence of or predisposition
CC to, or preventing or treating pathological conditions associated with an
CC ORFX-associated disorder. The nucleic acids can be used to express ORFX
CC proteins in gene therapy vectors. The proteins and nucleic acids may be
CC used to treat cancers, proliferative disorders, neurodegenerative
CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
CC storage, systemic lupus erythematosus, severe combined immunodeficiency
CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
CC cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
CC enhance coagulation; to inhibit thrombosis; and as a contraceptive
XX
SQ Sequence 138 AA;

Query Match 77.3%; Score 34; DB 3; Length 138;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          4 CXPXTGC 10
              | | |||
Db         15 CGPRTGC 21
```

Search completed: January 12, 2005, 23:10:52
Job time : 150.9 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 12, 2005, 23:04:08 ; Search time 16.8 Seconds
(without alignments)
40.090 Million cell updates/sec

Title: US-09-932-322-8
Perfect score: 38
Sequence: 1 CXPXTGC 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	36	94.7	601	2	A27020	DIF-induced presta
2	34	89.5	145	2	S07983	phospholipase A2 h
3	34	89.5	312	2	T05348	hypothetical prote
4	33	86.8	1058	2	T50496	hypothetical prote
5	32	84.2	64	2	F96006	hypothetical prote
6	31	81.6	482	2	T48397	S-receptor kinase-
7	31	81.6	643	2	T25473	hypothetical prote
8	30	78.9	129	2	A24255	chorion class A pr
9	30	78.9	132	2	B24255	chorion class A pr
10	30	78.9	151	2	AB0331	sigma E factor reg
11	30	78.9	199	2	T49486	hypothetical prote
12	30	78.9	200	2	S04926	wound-induced prot
13	30	78.9	201	2	T07729	wound-induced prot
14	30	78.9	211	2	T04098	CBP20 preproprotei
15	30	78.9	211	2	S04927	wound-induced prot
16	30	78.9	222	1	WMVZB4	antithrombin-III h
17	30	78.9	224	2	E84326	hypothetical prote
18	30	78.9	336	2	A83801	ABC transporter (s
19	30	78.9	345	1	WMVZW2	antithrombin-III h
20	30	78.9	406	2	T23898	hypothetical prote
21	30	78.9	430	2	T23899	hypothetical prote
22	30	78.9	551	2	S01793	arylsulfatase (EC
23	30	78.9	551	2	S07089	arylsulfatase (EC
24	30	78.9	648	2	T23864	hypothetical prote
25	30	78.9	1722	2	E89753	protein F11C7.4 [i
26	29	76.3	46	2	H71262	hypothetical prote
27	29	76.3	119	2	B45937	early chorion prot
28	29	76.3	119	2	S24292	chorion protein -
29	29	76.3	119	2	S24294	chorion protein -
30	29	76.3	119	2	S24291	chorion protein -
31	29	76.3	121	2	S24293	chorion class CA p
32	29	76.3	147	2	E82523	hypothetical prote
33	29	76.3	163	2	T33130	hypothetical prote
34	29	76.3	245	2	F84680	hypothetical prote
35	29	76.3	333	2	F90172	hypothetical prote
36	29	76.3	348	2	T35248	probable oxidoredu
37	29	76.3	375	2	A83636	hypothetical prote
38	29	76.3	379	2	S14885	hypothetical prote
39	29	76.3	449	2	E96676	hypothetical prote
40	29	76.3	507	2	T23375	hypothetical prote
41	29	76.3	513	2	D88991	protein apx-1 [imp
42	29	76.3	685	2	JC7570	Delta-4 protein -
43	29	76.3	686	2	JC7569	Delta-4 protein -
44	29	76.3	753	2	T28787	hypothetical prote
45	29	76.3	843	1	A27340	complement C7 prec

ALIGNMENTS

RESULT 1
A27020
DIF-induced prestalk pDd63 protein precursor - slime mold (Dictyostelium discoideum) (f
C;Species: Dictyostelium discoideum
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: A27020
R;Williams, J.G.; Ceccarelli, A.; McRobbie, S.; Mahbubani, H.; Kay, R.R.; Early, A.; Be
Cell 49, 185-192, 1987
A;Title: Direct induction of Dictyostelium prestalk gene expression by DIF provides evi
A;Reference number: A27020; MUID:87187613; PMID:3568124
A;Accession: A27020
A;Molecule type: DNA
A;Residues: 1-601 <WIL>
A;Cross-references: UNIPROT:Q7M4J3
C;Genetics:
A;Gene: pDd63
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-601/Product: DIF-induced prestalk pDd63 protein #status predicted <MAT>

Query Match 94.7%; Score 36; DB 2; Length 601;
Best Local Similarity 71.4%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 CXPXTGC 7
              | | |||
Db        245 CSPSTGC 251
```

RESULT 2
S07983
phospholipase A2 homolog precursor - common tiger snake
C;Species: Notechis scutatus scutatus (common tiger snake, mainland tiger snake)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: S07983
R;Ducancel, F.
submitted to the EMBL Data Library, January 1989
A;Reference number: S07983
A;Accession: S07983
A;Molecule type: mRNA
A;Residues: 1-145 <DUC>
A;Cross-references: UNIPROT:P20146; EMBL:X14043; NID:g64109; PIDN:CAA32201.1; PID:g6411
C;Superfamily: phospholipase A2
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-145/Product: phospholipase A2 #status predicted <MAT>

Query Match 89.5%; Score 34; DB 2; Length 145;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 CXPXTGC 7
              | | |||
Db        105 CDPETGC 111
```

RESULT 3
T05348
hypothetical protein F8B4.80 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T05348
R;Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; De
ewes, H.W.; Mayer, K.F.X.; Schueller, C.
submitted to the Protein Sequence Database, February 1999
A;Reference number: Z15409
A;Accession: T05348
A;Molecule type: DNA
A;Residues: 1-312 <BEV>
A;Cross-references: UNIPROT:Q9SUV3; EMBL:AL034567
A;Experimental source: cultivar Columbia; BAC clone F8B4
C;Genetics:
A;Map position: 4
A;Introns: 1/3; 44/3; 101/3; 139/3; 180/3
A;Note: F8B4.80

Query Match 89.5%; Score 34; DB 2; Length 312;
Best Local Similarity 71.4%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CXPXTGC 7
| | |||
Db 208 CDPNTGC 214

RESULT 4
T50496
hypothetical protein T22D6.50 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C;Accession: T50496
R;Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; De
ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25101
A;Accession: T50496
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1058 <BEV>
A;Cross-references: UNIPROT:Q9LEZ5; EMBL:AL357612
A;Experimental source: cultivar Columbia; BAC clone T22D6
C;Genetics:
A;Map position: 5
A;Introns: 60/3; 195/3; 222/3; 448/3; 492/3; 526/3; 555/2; 591/2; 616/3; 662/2; 715/3; 7
A;Note: T22D6.50

Query Match 86.8%; Score 33; DB 2; Length 1058;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CXPXTGC 7
| | |||
Db 1019 CPPETGC 1025

RESULT 5
F96006
hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymB
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: F96006
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: F96006
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-64 <KUR>
A;Cross-references: UNIPROT:Q92U25; GB:AL591985; PIDN:CAC49718.1; PID:g15141205; GSPDB:
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: SMb21688
A;Genome: plasmid

Query Match 84.2%; Score 32; DB 2; Length 64;
Best Local Similarity 57.1%; Pred. No. 22;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CXPXTGC 7
| | :||
Db 15 CAPSSGC 21

RESULT 6
T48397
S-receptor kinase-like protein - Arabidopsis thaliana
N;Alternate names: protein F17C15.120
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T48397
R;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.
submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24492
A;Accession: T48397
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-482 <BEV>
A;Cross-references: UNIPROT:Q9LZR8; EMBL:AL162506
A;Experimental source: cultivar Columbia; BAC clone F17C15
C;Genetics:
A;Map position: 5
A;Note: F17C15.120

Query Match 81.6%; Score 31; DB 2; Length 482;
Best Local Similarity 57.1%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CXPXTGC 7
| | :||
Db 301 CTPGSGC 307

RESULT 7
T25473
hypothetical protein B0507.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25473
R;Bradshaw, H.
submitted to the EMBL Data Library, July 1996
A;Description: The sequence of C. elegans cosmid B0507.
A;Reference number: Z20039
A;Accession: T25473
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-643 <BRA>
A;Cross-references: UNIPROT:Q22886; EMBL:U64833; PIDN:AAB04822.1; GSPDB:GN00023; CESP:B
A;Experimental source: strain Bristol N2; clone B0507
C;Genetics:
A;Gene: CESP:B0507.1

A;Map position: 5
A;Introns: 59/3; 133/1; 464/3; 586/1

Query Match 81.6%; Score 31; DB 2; Length 643;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 CXPXTGC 7
              | | :||
Db        209 CSPQSGC 215
```

RESULT 8
A24255
chorion class A protein L11 precursor - silkworm
C;Species: Bombyx mori (silkworm)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C;Accession: A24255
R;Spoerel, N.; Nguyen, H.T.; Kafatos, F.C.
J. Mol. Biol. 190, 23-35, 1986
A;Title: Gene regulation and evolution in the chorion locus of Bombyx mori. Structural a
A;Reference number: A92929; MUID:87060979; PMID:3023635
A;Accession: A24255
A;Molecule type: DNA
A;Residues: 1-129 <SPO>
A;Cross-references: UNIPROT:P08826; GB:X15557; GB:X04028; GB:X04029; GB:X04030; GB:X0403
C;Superfamily: chorion class A protein pc292
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-129/Product: chorion class A protein L11 #status predicted <MAT>

Query Match 78.9%; Score 30; DB 2; Length 129;
Best Local Similarity 57.1%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 CXPXTGC 7
              | |  ||
Db        116 CAPTCGC 122
```

RESULT 9
B24255
chorion class A protein L12 precursor - silkworm
C;Species: Bombyx mori (silkworm)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C;Accession: B24255
R;Spoerel, N.; Nguyen, H.T.; Kafatos, F.C.
J. Mol. Biol. 190, 23-35, 1986
A;Title: Gene regulation and evolution in the chorion locus of Bombyx mori. Structural a
A;Reference number: A92929; MUID:87060979; PMID:3023635
A;Accession: B24255
A;Molecule type: DNA
A;Residues: 1-132 <SPO>
A;Cross-references: UNIPROT:P08825; GB:X15557; GB:X04028; GB:X04029; GB:X04030; GB:X0403
C;Superfamily: chorion class A protein pc292
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-132/Product: chorion class A protein L12 #status predicted <MAT>

Query Match 78.9%; Score 30; DB 2; Length 132;
Best Local Similarity 57.1%; Pred. No. 90;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 CXPXTGC 7
              | |  ||
Db        117 CAPTCGC 123
```

RESULT 10
AB0331
sigma E factor regulatory protein rseC [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB0331
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AB0331
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-151 <KUR>
A;Cross-references: UNIPROT:Q8ZD76; GB:AL590842; PIDN:CAC92953.1; PID:g15980692; GSPDB:
C;Genetics:
A;Gene: rseC
C;Superfamily: Escherichia coli sigma-E factor regulatory protein rseC

Query Match 78.9%; Score 30; DB 2; Length 151;
Best Local Similarity 57.1%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 CXPXTGC 7
              | | :||
Db         20 CEPHSGC 26
```

RESULT 11
T49486
hypothetical protein B14D6.380 [imported] - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
C;Accession: T49486
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura
submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25022
A;Accession: T49486
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-199 <SCH>
A;Cross-references: EMBL:AL356173; GSPDB:GN00116; NCSP:B14D6.380
A;Experimental source: BAC clone B14D6; strain OR74A
C;Genetics:
A;Gene: NCSP:B14D6.380
A;Map position: 6
C;Superfamily: Neurospora crassa hypothetical protein B14D6.380

Query Match 78.9%; Score 30; DB 2; Length 199;
Best Local Similarity 57.1%; Pred. No. 1.2e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 CXPXTGC 7
              | | :||
Db        155 CKPLSGC 161
```

RESULT 12
S04926
wound-induced protein 1 precursor - potato
C;Species: Solanum tuberosum (potato)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: S04926
R;Stanford, A.; Bevan, M.; Northcote, D.
Mol. Gen. Genet. 215, 200-208, 1989
A;Title: Differential expression within a family of novel wound-induced genes in potato
A;Reference number: S04926; MUID:89218921; PMID:2710099
A;Accession: S04926
A;Molecule type: DNA
A;Residues: 1-200 <STA>
A;Cross-references: UNIPROT:P09761; EMBL:X13497; NID:g21617; PIDN:CAA31851.1; PID:g2161
C;Genetics:
A;Gene: win1
A;Introns: 143/3
C;Superfamily: hevein precursor; barwin homology; hevein chitin-binding domain homology
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-200/Product: wound-induced protein 1 #status predicted <MAT>
F;26-69/Domain: hevein chitin-binding domain homology <HCB>

```
F;78-199/Domain: barwin homology <BAR>

  Query Match             78.9%;  Score 30;  DB 2;  Length 200;
  Best Local Similarity   57.1%;  Pred. No. 1.2e+02;
  Matches    4;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CXPXTGC 7
              | |  ||
Db         56 CSPSQGC 62


RESULT 13
T07729
wound-induced protein (clone TAB7) - tomato (fragment)
C;Species: Lycopersicon esculentum (tomato)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C;Accession: T07729
R;Harris, N.; Taylor, J.E.; Roberts, J.A.
J. Exp. Bot. 48, 1223-1227, 1997
A;Title: Characterization and expression of an mRNA encoding a wound-induced (win) prote
A;Reference number: Z16099
A;Accession: T07729
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-201 <HAR>
A;Cross-references: UNIPROT:O03994; EMBL:U89764; NID:g1888560; PIDN:AAB49688.1; PID:g188
A;Experimental source: strain Ailsa craig; leaf abscission zone tissue
C;Superfamily: hevein precursor; barwin homology; hevein chitin-binding domain homology
F;16-60/Domain: hevein chitin-binding domain homology <HCB>
F;68-188/Domain: barwin homology <BAR>

  Query Match             78.9%;  Score 30;  DB 2;  Length 201;
  Best Local Similarity   57.1%;  Pred. No. 1.2e+02;
  Matches    4;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CXPXTGC 7
              | |  ||
Db         46 CSPSQGC 52


RESULT 14
T04098
CBP20 preproprotein - common tobacco
N;Alternate names: wound-induced protein
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04098
R;Ponstein, A.S.; Bres-Vloemans, S.A.; Sela-Buurlage, M.B.; Elzen, P.J.; Melchers, L.S.;
Plant Physiol. 104, 109-118, 1994
A;Title: A novel pathogen- and wound-inducible tobacco (Nicotiana tabacum) protein with
A;Reference number: Z15209; MUID:94159785; PMID:8115541
A;Accession: T04098
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-211 <PON>
A;Cross-references: UNIPROT:Q41231; EMBL:S72452; NID:g632733; PIDN:AAB29959.1; PID:g6327
A;Experimental source: cultivar Samsun NN
C;Superfamily: hevein precursor; barwin homology; hevein chitin-binding domain homology
F;23-66/Domain: hevein chitin-binding domain homology <HCB>
F;78-199/Domain: barwin homology <BAR>

  Query Match             78.9%;  Score 30;  DB 2;  Length 211;
  Best Local Similarity   57.1%;  Pred. No. 1.3e+02;
  Matches    4;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CXPXTGC 7
              | |  ||
Db         53 CSPSQGC 59


RESULT 15
S04927
wound-induced protein 2 precursor - potato
C;Species: Solanum tuberosum (potato)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: S04927
R;Stanford, A.; Bevan, M.; Northcote, D.
Mol. Gen. Genet. 215, 200-208, 1989
A;Title: Differential expression within a family of novel wound-induced genes in potato
A;Reference number: S04926; MUID:89218921; PMID:2710099
A;Accession: S04927
A;Molecule type: DNA
A;Residues: 1-211 <STA>
A;Cross-references: UNIPROT:P09762; EMBL:X13497; NID:g21617; PIDN:CAA31852.1; PID:g2161
C;Genetics:
A;Gene: win2
A;Introns: 142/3
C;Superfamily: hevein precursor; barwin homology; hevein chitin-binding domain homology
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-211/Product: wound-induced protein 2 #status predicted <MAT>
F;26-69/Domain: hevein chitin-binding domain homology <HCB>
F;77-198/Domain: barwin homology <BAR>

  Query Match             78.9%;  Score 30;  DB 2;  Length 211;
  Best Local Similarity   57.1%;  Pred. No. 1.3e+02;
  Matches    4;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CXPXTGC 7
              | |  ||
Db         56 CSPSQGC 62


Search completed: January 12, 2005, 23:16:03
Job time : 16.8 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 12, 2005, 22:56:08 ; Search time 88.55 Seconds
(without alignments)
45.484 Million cell updates/sec

Title: US-09-932-322-8
Perfect score: 38
Sequence: 1 CXPXTGC 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	36	94.7	192	2	Q98AR9	Q98ar9 rhizobium l
2	36	94.7	360	2	Q86AK7	Q86ak7 dictyosteli
3	36	94.7	546	2	Q8KJ72	Q8kj72 rhizobium l
4	36	94.7	601	2	Q7M4J3	Q7m4j3 dictyosteli
5	35	92.1	148	2	Q9N018	Q9n018 macaca fasc
6	35	92.1	148	2	Q95KD2	Q95kd2 macaca fasc
7	35	92.1	571	2	Q9AQP5	Q9aqp5 pseudomonas
8	34	89.5	113	2	Q7Z6J7	Q7z6j7 homo sapien
9	34	89.5	145	1	PA2X_NOTSC	P20146 notechis sc
10	34	89.5	167	2	Q7U7V9	Q7u7v9 synechococc
11	34	89.5	312	2	Q9SUV3	Q9suv3 arabidopsis
12	34	89.5	465	2	Q6TVH9	Q6tvh9 bovine papu
13	34	89.5	465	2	AAR98366	Aar98366 bovine pa
14	34	89.5	574	2	Q8LJ36	Q8lj36 oryza sativ
15	34	89.5	998	2	Q869K4	Q869k4 dictyosteli
16	34	89.5	2217	2	Q6Y625	Q6y625 lassa virus
17	34	89.5	2217	2	AAO59515	Aao59515 lassa vir
18	33	86.8	464	2	Q7XV21	Q7xv21 oryza sativ
19	33	86.8	1058	2	Q9LEZ5	Q9lez5 arabidopsis
20	33	86.8	1468	2	Q80TF6	Q80tf6 mus musculu
21	32	84.2	64	2	Q92U25	Q92u25 rhizobium m
22	32	84.2	123	2	Q926M4	Q926m4 listeria in
23	32	84.2	520	2	Q6Z8K1	Q6z8k1 oryza sativ
24	32	84.2	520	2	BAD15642	Bad15642 oryza sat
25	32	84.2	1152	2	Q9FI26	Q9fi26 arabidopsis
26	31	81.6	162	2	Q9WU17	Q9wu17 mesocricetu
27	31	81.6	166	2	Q8T4I5	Q8t4i5 drosophila
28	31	81.6	239	2	Q93KV9	Q93kv9 streptomyce
29	31	81.6	342	2	Q6VMH4	Q6vmh4 streptomyce
30	31	81.6	342	2	AAR30165	Aar30165 streptomy
31	31	81.6	361	2	Q8ECT9	Q8ect9 shewanella
32	31	81.6	482	2	Q9LZR8	Q9lzr8 arabidopsis
33	31	81.6	615	2	Q22886	Q22886 caenorhabdi
34	30	78.9	66	2	Q7N375	Q7n375 photorhabdu
35	30	78.9	78	2	P90569	P90569 plasmodium
36	30	78.9	95	2	P77130	P77130 escherichia
37	30	78.9	100	1	CHA3_BOMMO	P08929 bombyx mori
38	30	78.9	114	2	Q8MQ78	Q8mq78 caenorhabdi
39	30	78.9	119	2	Q8P958	Q8p958 xanthomonas
40	30	78.9	129	1	CHA1_BOMMO	P08826 bombyx mori
41	30	78.9	132	1	CHA2_BOMMO	P08825 bombyx mori
42	30	78.9	133	2	Q9LIW4	Q9liw4 oryza sativ
43	30	78.9	150	2	Q6D216	Q6d216 erwinia car
44	30	78.9	151	2	Q8ZD76	Q8zd76 yersinia pe
45	30	78.9	151	2	AAS62716	Aas62716 yersinia

ALIGNMENTS

RESULT 1
Q98AR9
ID Q98AR9 PRELIMINARY; PRT; 192 AA.
AC Q98AR9;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mlr5880 protein.
GN OrderedLocusNames=mlr5880;
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082936; PubMed=11214974;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti (supplement).";
RL DNA Res. 7:381-406(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003007; BAB52253.1; -.
DR HSSP; Q9ZFY9; 1FK8.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR002347; Adh_short_C2.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00081; GDHRDH.
KW Complete proteome.
SQ SEQUENCE 192 AA; 20183 MW; FD2F660D156037BC CRC64;

Query Match 94.7%; Score 36; DB 2; Length 192;
Best Local Similarity 71.4%; Pred. No. 27;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CXPXTGC 7
| | |||

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Db        176 CSPATGC 182


RESULT 2
Q86AK7
ID   Q86AK7      PRELIMINARY;      PRT;   360 AA.
AC   Q86AK7;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Similar to Dictyostelium discoideum (Slime mold). Prestalk
DE   protein.
OS   Dictyostelium discoideum (Slime mold).
OC   Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX   NCBI_TaxID=44689;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=AX4;
RX   MEDLINE=22092622; PubMed=12097910;
RA   Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA   Lehmann R., Baumgart C., Parra G., April J.P., Guigo R., Kumpf K.,
RA   Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT   "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RL   Nature 418:79-85(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=AX4;
RA   Baumgart C.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC116984; AAO51380.1; -.
DR   HSSP; P01382; 1NTN.
DR   InterPro; IPR002172; LDL_receptor_A.
DR   InterPro; IPR001673; S_mold_repeat.
DR   Pfam; PF00526; Dicty_CTDC; 13.
DR   PRINTS; PR00261; LDLRECEPTOR.
SQ   SEQUENCE   360 AA;  38013 MW;  4B0061ABA26ED81E CRC64;

  Query Match             94.7%;  Score 36;  DB 2;  Length 360;
  Best Local Similarity   71.4%;  Pred. No. 49;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CXPXTGC 7
              | | |||
Db        211 CSPSTGC 217


RESULT 3
Q8KJ72
ID   Q8KJ72      PRELIMINARY;      PRT;   546 AA.
AC   Q8KJ72;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   PUTATIVE SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE PROTEIN.
GN   Name=msi329;
OS   Rhizobium loti (Mesorhizobium loti).
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Phyllobacteriaceae; Mesorhizobium.
OX   NCBI_TaxID=381;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=R7A;
RX   MEDLINE=21999272; PubMed=12003951;
RA   Sullivan J.T., Trzebiatowski J.R., Cruickshank R.W., Gouzy J.,
RA   Brown S.D., Elliot R.M., Fleetwood D.J., McCallum N.G., Rossbach U.,
RA   Stuart G.S., Weaver J.E., Webby R.J., de Bruijn F.J., Ronson C.W.;
RT   "Comparative sequence analysis of the symbiosis island of
RT   Mesorhizobium loti strain R7A.";
RL   J. Bacteriol. 184:3086-3095(2002).
CC   -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC       (SDR) family.
DR   EMBL; AL672114; CAD31361.1; -.
DR   HSSP; P50163; 2AE1.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0008152; P:metabolism; IEA.
DR   InterPro; IPR002198; ADH_short.
DR   InterPro; IPR002347; Adh_short_C2.
DR   Pfam; PF00106; adh_short; 2.
DR   PRINTS; PR00081; GDHRDH.
DR   PRINTS; PR00080; SDRFAMILY.
DR   PROSITE; PS00061; ADH_SHORT; 1.
KW   Oxidoreductase.
SQ   SEQUENCE   546 AA;  56900 MW;  091D2EFED8E55A9C CRC64;

  Query Match             94.7%;  Score 36;  DB 2;  Length 546;
  Best Local Similarity   71.4%;  Pred. No. 72;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CXPXTGC 7
              | | |||
Db        530 CSPATGC 536


RESULT 4
Q7M4J3
ID   Q7M4J3      PRELIMINARY;      PRT;   601 AA.
AC   Q7M4J3;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   DIF-induced prestalk pDd63 protein precursor (Fragments).
OS   Dictyostelium discoideum (Slime mold).
OC   Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX   NCBI_TaxID=44689;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87187613; PubMed=3568124;
RA   Williams J.G., Ceccarelli A., McRobbie S., Mahbubani H., Kay R.R.,
RA   Early A., Berks M., Jermyn K.A.;
RT   "Direct induction of Dictyostelium prestalk gene expression by DIF
RT   provides evidence that DIF is a morphogen.";
RL   Cell 49:185-192(1987).
DR   PIR; A27020; A27020.
DR   InterPro; IPR001673; S_mold_repeat.
DR   Pfam; PF00526; Dicty_CTDC; 19.
FT   NON_TER     601    601
SQ   SEQUENCE   601 AA;  63359 MW;  7D4433616CDAC438 CRC64;

  Query Match             94.7%;  Score 36;  DB 2;  Length 601;
  Best Local Similarity   71.4%;  Pred. No. 79;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CXPXTGC 7
              | | |||
Db        245 CSPSTGC 251


RESULT 5
Q9N018
ID   Q9N018      PRELIMINARY;      PRT;   148 AA.
AC   Q9N018;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Cerebellum cortex;
RA   Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA   Suzuki Y., Sugano S., Hashimoto K.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
```

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DR   EMBL; AB046629; BAB03547.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   148 AA;  15495 MW;  6242BCE430C6E13B CRC64;

  Query Match             92.1%;  Score 35;  DB 2;  Length 148;
  Best Local Similarity   71.4%;  Pred. No. 33;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CXPXTGC 7
              | | |||
Db         74 CGPSTGC 80


RESULT 6
Q95KD2
ID   Q95KD2      PRELIMINARY;      PRT;   148 AA.
AC   Q95KD2;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Medulla oblogata;
RA   Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA   Suzuki Y., Sugano S., Hashimoto K.;
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB062948; BAB60737.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   148 AA;  15473 MW;  C8D2AA301E0C8191 CRC64;

  Query Match             92.1%;  Score 35;  DB 2;  Length 148;
  Best Local Similarity   71.4%;  Pred. No. 33;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CXPXTGC 7
              | | |||
Db         74 CGPSTGC 80


RESULT 7
Q9AQP5
ID   Q9AQP5      PRELIMINARY;      PRT;   571 AA.
AC   Q9AQP5;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Putative ABC transporter subunit.
GN   Name=ORF31;
OS   Pseudomonas resinovorans.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=53412;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CA10;
RX   MEDLINE=97386424; PubMed=9244273;
RA   Sato S., Ouchiyama N., Kimura T., Nojiri H., Yamane H., Omori T.;
RT   "Cloning of genes involved in carbazole degradation of Pseudomonas sp.
RT   strain CA10: nucleotide sequence of genes and characterization of
RT   meta-cleavage enzymes and hydrolase.";
RL   J. Bacteriol. 179:4841-4849(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CA10;
RX   MEDLINE=97386425; PubMed=9244274;
RA   Sato S., Nam J., Kasuga K., Nojiri H., Yamane H., Omori T.;
RT   "Identification and characterization of genes encoding carbazole 1,9a-
RT   dioxygenase in Pseudomonas sp. strain CA10.";
RL   J. Bacteriol. 179:4850-4858(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CA10;
RX   MEDLINE=21264379; PubMed=11371531;
RA   Nojiri H., Sekiguchi H., Maeda K., Urata M., Nakai S., Yoshida T.,
RA   Habe H., Omori T.;
RT   "Genetic characterization and evolutionary implications of car gene
RT   cluster in carbazole-degrader, Pseudomonas sp. strain CA10.";
RL   J. Bacteriol. 183:3663-3679(2001).
DR   EMBL; AB047548; BAB32742.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR001851; Bac_inmem_transp.
DR   InterPro; IPR001865; Ribosomal_S2.
DR   Pfam; PF02653; BPD_transp_2; 2.
DR   PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
SQ   SEQUENCE   571 AA;  60653 MW;  9A8854777078C186 CRC64;

  Query Match             92.1%;  Score 35;  DB 2;  Length 571;
  Best Local Similarity   71.4%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CXPXTGC 7
              | | |||
Db        565 CGPSTGC 571


RESULT 8
Q7Z6J7
ID   Q7Z6J7      PRELIMINARY;      PRT;   113 AA.
AC   Q7Z6J7;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC053646; AAH53646.1; -.
KW   Hypothetical protein.
```

```
SQ   SEQUENCE   113 AA;  11613 MW;  8624A42297F4A3FF CRC64;

  Query Match             89.5%;  Score 34;  DB 2;  Length 113;
  Best Local Similarity   71.4%;  Pred. No. 40;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CXPXTGC 7
              | | |||
Db        103 CYPKTGC 109


RESULT 9
PA2X_NOTSC
ID   PA2X_NOTSC     STANDARD;      PRT;   145 AA.
AC   P20146;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Probable phospholipase A2 precursor (EC 3.1.1.4) (Phosphatidylcholine
DE   2-acylhydrolase).
OS   Notechis scutatus scutatus (Mainland tiger snake) (Common tiger
OS   snake).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Elapidae; Acanthophiinae; Notechis.
OX   NCBI_TaxID=70142;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RA   Ducancel F.;
RL   Submitted (JAN-1989) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
CC       acyl groups in 3-sn-phosphoglycerides.
CC   -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC       acylglycerophosphocholine + a carboxylate.
CC   -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the phospholipase A2 family. Group I
CC       subfamily.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X14043; CAA32201.1; -.
DR   PIR; S07983; S07983.
DR   HSSP; P00608; 1AE7.
DR   InterPro; IPR001211; PhospholipaseA2.
DR   Pfam; PF00068; Phospholip_A2_1; 1.
DR   PRINTS; PR00389; PHPHLIPASEA2.
DR   ProDom; PD000303; PhospholipaseA2; 1.
DR   SMART; SM00085; PA2c; 1.
DR   PROSITE; PS00119; PA2_ASP; 1.
DR   PROSITE; PS00118; PA2_HIS; 1.
KW   Calcium; Hydrolase; Lipid degradation; Multigene family; Signal.
FT   SIGNAL        1     21       Potential.
FT   PROPEP       22     27       Potential.
FT   CHAIN        28    145       Probable phospholipase A2.
FT   ACT_SITE     75     75       By similarity.
FT   ACT_SITE    119    119       By similarity.
FT   DISULFID     38     98       By similarity.
FT   DISULFID     54    144       By similarity.
FT   DISULFID     56     72       By similarity.
FT   DISULFID     71    125       By similarity.
FT   DISULFID     78    118       By similarity.
FT   DISULFID     87    111       By similarity.
FT   DISULFID    105    116       By similarity.
FT   METAL        55     55       Calcium (via carbonyl oxygen) (By
FT                                similarity).
FT   METAL        57     57       Calcium (via carbonyl oxygen) (By
FT                                similarity).
FT   METAL        76     76       Calcium (By similarity).
SQ   SEQUENCE   145 AA;  16002 MW;  38E36029AEE5FAC9 CRC64;

  Query Match             89.5%;  Score 34;  DB 1;  Length 145;
  Best Local Similarity   71.4%;  Pred. No. 50;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CXPXTGC 7
              | | |||
Db        105 CDPETGC 111


RESULT 10
Q7U7V9
ID   Q7U7V9      PRELIMINARY;      PRT;   167 AA.
AC   Q7U7V9;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical precursor.
GN   OrderedLocusNames=SYNW0871;
OS   Synechococcus sp. (strain WH8102).
OC   Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX   NCBI_TaxID=84588;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22825697; PubMed=12917641; DOI=10.1038/nature01943;
RA   Palenik B., Brahamsha B., Larimer F.W., Land M.L., Hauser L.,
RA   Chain P., Lamerdin J.E., Regala W., Allen E.E., McCarren J.,
RA   Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.;
RT   "The genome of a motile marine Synechococcus.";
RL   Nature 424:1037-1042(2003).
DR   EMBL; BX569691; CAE07386.1; -.
KW   Complete proteome; Hypothetical protein; Signal.
FT   SIGNAL        1     22       Potential.
SQ   SEQUENCE   167 AA;  18419 MW;  0B3AFB830ECF971C CRC64;

  Query Match             89.5%;  Score 34;  DB 2;  Length 167;
  Best Local Similarity   71.4%;  Pred. No. 58;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CXPXTGC 7
              | | |||
Db        133 CYPGTGC 139


RESULT 11
Q9SUV3
ID   Q9SUV3      PRELIMINARY;      PRT;   312 AA.
AC   Q9SUV3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein F8B4.80 (Hypothetical protein AT4g32380).
GN   Name=F8B4.80; Synonyms=AT4g32380;
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bevan M., Terryn N., Ardiles W., Buysshaert C., Dasseville R.,
RA   De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,
RA   Villaroel R., Gielen J., Van Montagu M., Hoheisel J., Mewes H.W.,
RA   Mayer K.F.X., Lemcke K., Schueller C.;
RL   Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   EU Arabidopsis sequencing project;
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
```

```
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Terryn N., Ardiles W., Buysshaert C., Dasseville R., De Clerck R.,
RA   De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villaroel R.,
RA   Gielen J., Van Montagu M., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   EU Arabidopsis sequencing project;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to family 28 of glycosyl hydrolases.
DR   EMBL; AL034567; CAA22565.1; -.
DR   EMBL; AL161581; CAB79955.1; -.
DR   PIR; T05348; T05348.
DR   GO; GO:0004650; F:polygalacturonase activity; IEA.
DR   GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR   InterPro; IPR000743; Glyco_hydro_28.
DR   InterPro; IPR006626; PbH1.
DR   InterPro; IPR011050; Pectin_lyas_like.
DR   Pfam; PF00295; Glyco_hydro_28; 2.
DR   SMART; SM00710; PbH1; 3.
KW   Cell wall; Glycosidase; Hydrolase; Hypothetical protein.
SQ   SEQUENCE   312 AA;  34095 MW;  E2E70A2622F30EE0 CRC64;

  Query Match             89.5%;  Score 34;  DB 2;  Length 312;
  Best Local Similarity   71.4%;  Pred. No. 1e+02;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CXPXTGC 7
              | | |||
Db        208 CDPNTGC 214


RESULT 12
Q6TVH9
ID   Q6TVH9      PRELIMINARY;      PRT;   465 AA.
AC   Q6TVH9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Bovine papular stomatitis virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Parapoxvirus.
OX   NCBI_TaxID=129727;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BV-AR02;
RX   PubMed=14671098;
RA   Delhon G., Tulman E.R., Afonso C.L., Lu Z.,
RA   de la Concha-Bermejillo A., Lehmkuhl H.D., Piccone M.E., Kutish G.F.,
RA   Rock D.L.;
RT   "Genomes of the Parapoxviruses Orf Virus and Bovine Papular
RT   Stomtatitis Virus.";
RL   J. Virol. 78:168-177(2004).
DR   EMBL; AY386265; AAR98366.1; -.
DR   InterPro; IPR007027; Pox_F11.
DR   Pfam; PF04943; Pox_F11; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   465 AA;  51404 MW;  BD735469CBED1B79 CRC64;

  Query Match             89.5%;  Score 34;  DB 2;  Length 465;
  Best Local Similarity   71.4%;  Pred. No. 1.5e+02;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CXPXTGC 7
              | | |||
Db         26 CVPRTGC 32


RESULT 13
AAR98366
ID   AAR98366    PRELIMINARY;      PRT;   465 AA.
AC   AAR98366;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Bovine papular stomatitis virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Parapoxvirus.
OX   NCBI_TaxID=129727;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BV-AR02;
RX   PubMed=14671098;
RA   Delhon G., Tulman E.R., Afonso C.L., Lu Z.,
RA   de la Concha-Bermejillo A., Lehmkuhl H.D., Piccone M.E., Kutish G.F.,
RA   Rock D.L.;
RT   "Genomes of the Parapoxviruses Orf Virus and Bovine Papular
RT   Stomtatitis Virus.";
RL   J. Virol. 78:168-177(2004).
DR   EMBL; AY386265; AAR98366.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   465 AA;  51404 MW;  BD735469CBED1B79 CRC64;

  Query Match             89.5%;  Score 34;  DB 2;  Length 465;
  Best Local Similarity   71.4%;  Pred. No. 1.5e+02;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CXPXTGC 7
              | | |||
Db         26 CVPRTGC 32


RESULT 14
Q8LJ36
ID   Q8LJ36      PRELIMINARY;      PRT;   574 AA.
AC   Q8LJ36;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   P0413G02.18 protein.
GN   Name=P0413G02.18;
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA   Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA   Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA   Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA   Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA   Ikeno M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
RA   Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA   Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA   Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA   Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K, Shibata M.,
RA   Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA   Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA   Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA   Yano M., Jiang J., Gojobori T.;
RT   "The genome sequence and structure of rice chromosome 1.";
RL   Nature 420:312-316(2002).
DR   EMBL; AP003344; BAC07361.1; -.
DR   HSSP; P20142; 1AVF.
DR   Gramene; Q8LJ36; -.
DR   GO; GO:0004194; F:pepsin A activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001461; Peptidase_A1.
DR   InterPro; IPR009007; Pept_Aspartic.
DR   Pfam; PF00026; Asp; 1.
DR   PRINTS; PR00792; PEPSIN.
```

```
SQ   SEQUENCE   574 AA;  60980 MW;  A2D654446084F35F CRC64;

  Query Match             89.5%;  Score 34;  DB 2;  Length 574;
  Best Local Similarity   71.4%;  Pred. No. 1.9e+02;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CXPXTGC 7
              | | |||
Db        119 CSPCTGC 125


RESULT 15
Q869K4
ID   Q869K4      PRELIMINARY;      PRT;   998 AA.
AC   Q869K4;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Similar to Mus musculus (Mouse). Tenascin X.
OS   Dictyostelium discoideum (Slime mold).
OC   Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX   NCBI_TaxID=44689;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=AX4;
RX   MEDLINE=22092622; PubMed=12097910;
RA   Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA   Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA   Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT   "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RL   Nature 418:79-85(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=AX4;
RA   Baumgart C.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC115598; AAO53206.1; -.
DR   HSSP; P01132; 1EGF.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR000742; EGF_2.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR006210; IEGF.
DR   InterPro; IPR002049; Laminin_EGF.
DR   Pfam; PF00008; EGF; 7.
DR   PRINTS; PR00011; EGFLAMININ.
DR   SMART; SM00181; EGF; 9.
DR   PROSITE; PS00022; EGF_1; UNKNOWN_10.
DR   PROSITE; PS01186; EGF_2; 7.
DR   PROSITE; PS50026; EGF_3; 6.
SQ   SEQUENCE   998 AA;  106001 MW;  F79BEF394D3E2369 CRC64;

  Query Match             89.5%;  Score 34;  DB 2;  Length 998;
  Best Local Similarity   71.4%;  Pred. No. 3.1e+02;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CXPXTGC 7
              | | |||
Db        609 CNPFTGC 615


Search completed: January 12, 2005, 23:15:11
Job time : 88.55 secs
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Nothing

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 12, 2005, 22:55:47 ; Search time 79.1 Seconds
(without alignments)
31.746 Million cell updates/sec

Title: US-09-932-322-8
Perfect score: 38
Sequence: 1 CXPXTGC 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	35	92.1	79	4	AAU49413	Aau49413 Propionib
2	35	92.1	79	6	ABM45932	Abm45932 Propionib
3	35	92.1	180	7	ABO74428	Abo74428 Pseudomon
4	34	89.5	7	3	AAY62764	Aay62764 PB-cadher
5	34	89.5	7	3	AAY61489	Aay61489 Cadherin-
6	34	89.5	7	3	AAY62007	Aay62007 Cadherin-
7	34	89.5	7	3	AAY62224	Aay62224 Cadherin-
8	34	89.5	7	5	ABJ00550	Abj00550 B lymphoc
9	34	89.5	7	5	ABG33862	Abg33862 B Lymphoc
10	34	89.5	13	5	ABJ00545	Abj00545 B lymphoc
11	34	89.5	13	5	ABG33861	Abg33861 B Lymphoc
12	34	89.5	53	4	AAU44932	Aau44932 Propionib
13	34	89.5	53	6	ABM41451	Abm41451 Propionib
14	34	89.5	113	6	ADA54961	Ada54961 Human pro
15	34	89.5	138	3	AAB42027	Aab42027 Human ORF
16	34	89.5	250	7	ABO75329	Abo75329 Pseudomon
17	34	89.5	312	5	ABB93198	Abb93198 Herbicida
18	34	89.5	540	7	ADF05702	Adf05702 Bacterial
19	34	89.5	3226	4	ABG28408	Abg28408 Novel hum
20	33	86.8	158	4	AAU40006	Aau40006 Propionib
21	33	86.8	158	6	ABM36525	Abm36525 Propionib
22	32	84.2	751	3	AAG43626	Aag43626 Arabidops
23	32	84.2	798	3	AAG43625	Aag43625 Arabidops
24	32	84.2	835	3	AAG43624	Aag43624 Arabidops
25	31	81.6	7	3	AAY63264	Aay63264 Protocadh
26	31	81.6	90	7	ABO81251	Abo81251 Pseudomon
27	31	81.6	114	5	ABP06368	Abp06368 Human ORF
28	31	81.6	148	7	ADJ71040	Adj71040 Human hea
29	31	81.6	183	7	ADF58925	Adf58925 Human pol
30	31	81.6	193	4	AAO00015	Aao00015 Human pol
31	31	81.6	193	7	ADF60298	Adf60298 Human con
32	31	81.6	238	6	ABP99259	Abp99259 Orthosomy
33	31	81.6	239	6	ABP99348	Abp99348 Orthosomy
34	31	81.6	239	6	ABP76713	Abp76713 Streptomy
35	31	81.6	310	7	ABO74638	Abo74638 Pseudomon
36	31	81.6	444	7	ABO70819	Abo70819 Pseudomon
37	31	81.6	482	5	ABB93340	Abb93340 Herbicida
38	31	81.6	580	2	AAW32363	Aaw32363 Mycobacte
39	31	81.6	580	2	AAW32431	Aaw32431 Mycobacte
40	31	81.6	580	2	AAW64303	Aaw64303 Mycobacte
41	31	81.6	580	2	AAW81666	Aaw81666 M. tuberc
42	31	81.6	580	2	AAY38968	Aay38968 M. tuberc
43	31	81.6	580	2	AAY39105	Aay39105 M. tuberc
44	31	81.6	602	2	AAY04996	Aay04996 Mycobacte
45	31	81.6	638	2	AAY04992	Aay04992 Mycobacte

ALIGNMENTS

RESULT 1
AAU49413
ID AAU49413 standard; protein; 79 AA.
XX
AC AAU49413;
XX
DT 13-FEB-2002 (first entry)
XX
DE Propionibacterium acnes immunogenic protein #10309.
XX
KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX
OS Propionibacterium acnes.
XX
PN WO200181581-A2.
XX
PD 01-NOV-2001.
XX
PF 20-APR-2001; 2001WO-US012865.
XX
PR 21-APR-2000; 2000US-0199047P.
PR 02-JUN-2000; 2000US-0208841P.
PR 07-JUL-2000; 2000US-0216747P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
DR WPI; 2001-616774/71.
DR N-PSDB; AAS59545.
XX
PT Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris.
XX
PS Example 1; SEQ ID NO 10608; 1069pp; English.
XX
CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory

CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 79 AA;

Query Match 92.1%; Score 35; DB 4; Length 79;
Best Local Similarity 71.4%; Pred. No. 55;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CXPXTGC 7
| | |||
Db 3 CSPGTGC 9

RESULT 2
ABM45932
ID ABM45932 standard; protein; 79 AA.
XX
AC ABM45932;
XX
DT 20-OCT-2003 (first entry)
XX
DE Propionibacterium acnes predicted ORF-encoded polypeptide #10608.
XX
KW Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
KW immunostimulant; immune response; vaccine.
XX
OS Propionibacterium acnes.
XX
PN WO2003033515-A1.
XX
PD 24-APR-2003.
XX
PF 11-OCT-2002; 2002WO-US032727.
XX
PR 15-OCT-2001; 2001US-00978825.
XX
PA (CORI-) CORIXA CORP.
XX
PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
PI Barth B, Vallieve-Douglass J;
XX
DR WPI; 2003-381789/36.
DR N-PSDB; ACF64474.
XX
PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
PT or for stimulating an immune response specific for a P. acnes protein.
XX
PS Example 1; SEQ ID NO 10608; 1481pp; English.
XX
CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
CC encoding a Propionibacterium acnes protein. The invention also relates to
CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
CC immunogenic fragments of P. acnes polypeptides. The invention
CC additionally encompasses expression vectors and host cells comprising a
CC polynucleotide of the invention; antibodies against polypeptides of the
CC invention; fusion proteins comprising a polypeptide of the invention; a
CC method for stimulating an immune response specific for a P. acnes
CC polypeptide and an isolated T cell population comprising T cells prepared
CC via this method; a vaccine composition (comprising P. acnes polypeptides,
CC polynucleotides, antibodies, fusion proteins, T cell populations, or
CC antigen-presenting cells that express the polypeptide); a method and kit
CC for detecting or determining the presence or absence of P. acnes in a
CC patient; and a method for inhibiting the development of P. acnes in a
CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
CC proteins, T cell populations or antigen-presenting cells that express the
CC polypeptides are useful for diagnosing, preventing or treating acne
CC vulgaris, or for stimulating an immune response specific for a P. acnes
CC protein. The polynucleotides can also be used as probes or primers for
CC nucleic acid hybridisation. The vaccine composition is useful for the
CC stimulation of an immune response against P. acnes, or for treating acne,
CC and the kit is useful for performing a diagnostic assay. The present
CC sequence represents a polypeptide predicted to be encoded by an ORF (open
CC reading frame) contained within the P. acnes polynucleotides of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 79 AA;

Query Match 92.1%; Score 35; DB 6; Length 79;
Best Local Similarity 71.4%; Pred. No. 55;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CXPXTGC 7
| | |||
Db 3 CSPGTGC 9

RESULT 3
ABO74428
ID ABO74428 standard; protein; 180 AA.
XX
AC ABO74428;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polypeptide #6603.
XX
KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI; 2003-615309/58.
DR N-PSDB; ABD07999.
XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 23174; 455pp; English.
XX
CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant

CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABO67826-
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 180 AA;

Query Match 92.1%; Score 35; DB 7; Length 180;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CXPXTGC 7
| | |||
Db 124 CRPATGC 130

RESULT 4
AAY62764
ID AAY62764 standard; peptide; 7 AA.
XX
AC AAY62764;
XX
DT 02-MAR-2000 (first entry)
XX
DE PB-cadherin cell adhesion recognition cyclic peptide SEQ ID NO:4047.
XX
KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;
KW inhibition; cadherin extracellular domain; cell adhesion recognition;
KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
KW neurological disease; cyclic.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1. .7
XX
PN WO9957149-A2.
XX
PD 11-NOV-1999.
XX
PF 05-MAY-1999; 99WO-CA000363.
XX
PR 05-MAY-1998; 98US-00073040.
PR 06-NOV-1998; 98US-00187859.
PR 20-JAN-1999; 99US-00234395.
PR 08-MAR-1999; 99US-00264516.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuk OW, Gour BJ, Byers S;
XX
DR WPI; 2000-038791/03.
XX
PT New cadherin modulating agents, used for modulating nonclassical cadherin
PT -mediated functions for treating e.g. cancers, obesity, rheumatoid
PT arthritis, multiple sclerosis, diabetes or a neurological disease.
XX
PS Claim 72; Page 193; 252pp; English.
XX
CC The present invention describes cadherin modulating agents (MA)
CC comprising peptides which comprise a nonclassical cadherin cell adhesion
CC recognition (CAR) sequence. The MAs can be used for modulating
CC nonclassical cadherin-mediated functions. They can be used for e.g.
CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
CC mammal, enhancing delivery of a drug through the skin of a mammal,
CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
CC expressing cell, preventing or treating obesity in a mammal, stimulating
CC blood vessel regression in a mammal, enhancing drug delivery to the
CC central nervous system, treating a demyelinating neurological disease,
CC increasing vasopermeability in a mammal, enhancing adhesion of
CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
CC a mammal, or preventing pregnancy in a mammal. They can also be used for
CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
CC -related macular degeneration, multiple sclerosis and diabetes. The
CC products can also be used for detection and diagnosis and in bioreactors.
CC AAY60592 to AAY64572 represent specifically claimed peptides, and
CC AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in
CC the exemplification of the present invention
XX
SQ Sequence 7 AA;

Query Match 89.5%; Score 34; DB 3; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CXPXTGC 7
| | |||
Db 1 CDPKTGC 7

RESULT 5
AAY61489
ID AAY61489 standard; peptide; 7 AA.
XX
AC AAY61489;
XX
DT 02-MAR-2000 (first entry)
XX
DE Cadherin-7 cell adhesion recognition cyclic peptide SEQ ID NO:1375.
XX
KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;
KW inhibition; cadherin extracellular domain; cell adhesion recognition;
KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
KW neurological disease; cyclic.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1. .7
XX
PN WO9957149-A2.
XX
PD 11-NOV-1999.
XX
PF 05-MAY-1999; 99WO-CA000363.
XX
PR 05-MAY-1998; 98US-00073040.
PR 06-NOV-1998; 98US-00187859.
PR 20-JAN-1999; 99US-00234395.
PR 08-MAR-1999; 99US-00264516.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuk OW, Gour BJ, Byers S;
XX
DR WPI; 2000-038791/03.
XX
PT New cadherin modulating agents, used for modulating nonclassical cadherin

PT -mediated functions for treating e.g. cancers, obesity, rheumatoid
PT arthritis, multiple sclerosis, diabetes or a neurological disease.
XX
PS Claim 36; Page 172; 252pp; English.
XX
CC The present invention describes cadherin modulating agents (MA)
CC comprising peptides which comprise a nonclassical cadherin cell adhesion
CC recognition (CAR) sequence. The MAs can be used for modulating
CC nonclassical cadherin-mediated functions. They can be used for e.g.
CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
CC mammal, enhancing delivery of a drug through the skin of a mammal,
CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
CC expressing cell, preventing or treating obesity in a mammal, stimulating
CC blood vessel regression in a mammal, enhancing drug delivery to the
CC central nervous system, treating a demyelinating neurological disease,
CC increasing vasopermeability in a mammal, enhancing adhesion of
CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
CC a mammal, or preventing pregnancy in a mammal. They can also be used for
CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
CC -related macular degeneration, multiple sclerosis and diabetes. The
CC products can also be used for detection and diagnosis and in bioreactors.
CC AAY60592 to AAY64572 represent specifically claimed peptides, and
CC AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in
CC the exemplification of the present invention
XX
SQ Sequence 7 AA;

Query Match 89.5%; Score 34; DB 3; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CXPXTGC 7
| | |||
Db 1 CEPKTGC 7

RESULT 6
AAY62007
ID AAY62007 standard; peptide; 7 AA.
XX
AC AAY62007;
XX
DT 02-MAR-2000 (first entry)
XX
DE Cadherin-12 cell adhesion recognition cyclic peptide SEQ ID NO:1799.
XX
KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;
KW inhibition; cadherin extracellular domain; cell adhesion recognition;
KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
KW neurological disease; cyclic.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1. .7
XX
PN WO9957149-A2.
XX
PD 11-NOV-1999.
XX
PF 05-MAY-1999; 99WO-CA000363.
XX
PR 05-MAY-1998; 98US-00073040.
PR 06-NOV-1998; 98US-00187859.
PR 20-JAN-1999; 99US-00234395.
PR 08-MAR-1999; 99US-00264516.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuk OW, Gour BJ, Byers S;
XX
DR WPI; 2000-038791/03.
XX
PT New cadherin modulating agents, used for modulating nonclassical cadherin
PT -mediated functions for treating e.g. cancers, obesity, rheumatoid
PT arthritis, multiple sclerosis, diabetes or a neurological disease.
XX
PS Claim 48; Page 180; 252pp; English.
XX
CC The present invention describes cadherin modulating agents (MA)
CC comprising peptides which comprise a nonclassical cadherin cell adhesion
CC recognition (CAR) sequence. The MAs can be used for modulating
CC nonclassical cadherin-mediated functions. They can be used for e.g.
CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
CC mammal, enhancing delivery of a drug through the skin of a mammal,
CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
CC expressing cell, preventing or treating obesity in a mammal, stimulating
CC blood vessel regression in a mammal, enhancing drug delivery to the
CC central nervous system, treating a demyelinating neurological disease,
CC increasing vasopermeability in a mammal, enhancing adhesion of
CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
CC a mammal, or preventing pregnancy in a mammal. They can also be used for
CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
CC -related macular degeneration, multiple sclerosis and diabetes. The
CC products can also be used for detection and diagnosis and in bioreactors.
CC AAY60592 to AAY64572 represent specifically claimed peptides, and
CC AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in
CC the exemplification of the present invention
XX
SQ Sequence 7 AA;

Query Match 89.5%; Score 34; DB 3; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CXPXTGC 7
| | |||
Db 1 CDPKTGC 7

RESULT 7
AAY62224
ID AAY62224 standard; peptide; 7 AA.
XX
AC AAY62224;
XX
DT 02-MAR-2000 (first entry)
XX
DE Cadherin-14 cell adhesion recognition cyclic peptide SEQ ID NO:3971.
XX
KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;
KW inhibition; cadherin extracellular domain; cell adhesion recognition;
KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
KW neurological disease; cyclic.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers

```
FT   Disulfide-bond  1. .7
XX
PN   WO9957149-A2.
XX
PD   11-NOV-1999.
XX
PF   05-MAY-1999;   99WO-CA000363.
XX
PR   05-MAY-1998;   98US-00073040.
PR   06-NOV-1998;   98US-00187859.
PR   20-JAN-1999;   99US-00234395.
PR   08-MAR-1999;   99US-00264516.
XX
PA   (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI   Blaschuk OW,  Gour BJ,  Byers S;
XX
DR   WPI; 2000-038791/03.
XX
PT   New cadherin modulating agents, used for modulating nonclassical cadherin
PT   -mediated functions for treating e.g. cancers, obesity, rheumatoid
PT   arthritis, multiple sclerosis, diabetes or a neurological disease.
XX
PS   Claim 54; Page 184; 252pp; English.
XX
CC   The present invention describes cadherin modulating agents (MA)
CC   comprising peptides which comprise a nonclassical cadherin cell adhesion
CC   recognition (CAR) sequence. The MAs can be used for modulating
CC   nonclassical cadherin-mediated functions. They can be used for e.g.
CC   inhibiting adhesion of nonclassical-cadherin expressing cells in a
CC   mammal, enhancing delivery of a drug through the skin of a mammal,
CC   enhancing delivery of a drug to a tumour in a mammal, treating cancer in
CC   a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
CC   angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
CC   expressing cell, preventing or treating obesity in a mammal, stimulating
CC   blood vessel regression in a mammal, enhancing drug delivery to the
CC   central nervous system, treating a demyelinating neurological disease,
CC   increasing vasopermeability in a mammal, enhancing adhesion of
CC   nonclassical cadherin-expressing cells, inhibiting synaptic stability in
CC   a mammal, or preventing pregnancy in a mammal. They can also be used for
CC   e.g. enhancing or directing neurite outgrowth, facilitating wound healing
CC   or reducing scar tissue, or enhancing adhesion of foreign tissue in a
CC   mammal. They can also be used for treating e.g. psoriasis, arthritis, age
CC   -related macular degeneration, multiple sclerosis and diabetes. The
CC   products can also be used for detection and diagnosis and in bioreactors.
CC   AAY60592 to AAY64572 represent specifically claimed peptides, and
CC   AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in
CC   the exemplification of the present invention
XX
SQ   Sequence 7 AA;

  Query Match             89.5%;  Score 34;  DB 3;  Length 7;
  Best Local Similarity   71.4%;  Pred. No. 1.7e+06;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CXPXTGC 7
              | | |||
Db          1 CDPKTGC 7


RESULT 8
ABJ00550
ID   ABJ00550 standard; peptide; 7 AA.
XX
AC   ABJ00550;
XX
DT   05-SEP-2002  (first entry)
XX
DE   B lymphocyte stimulator protein binding peptide #1.
XX
KW   B lymphocyte stimulator protein binding protein; BLyS; immune disease;
KW   allergy; proliferative disease; infectious disease; arteriosclerosis;
KW   inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW   ischaemia; graft-versus-host disease; neurodegenerative disease;
KW   immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW   neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW   antiasthmatic; antiallergic; thyromimetic; antianaemic; haemostatic;
KW   dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW   antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 2
FT                   /label= Phe, Trp, Tyr
FT   Misc-difference 4
FT                   /label= Pro, Tyr
XX
PN   WO200216411-A2.
XX
PD   28-FEB-2002.
XX
PF   17-AUG-2001; 2001WO-US025850.
XX
PR   18-AUG-2000; 2000US-0226700P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Beltzer JP,  Potter DM,  Fleming TL,  Rosen CA;
XX
DR   WPI; 2002-499775/53.
XX
PT   The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT   administering B Lymphocyte stimulator binding polypeptide.
XX
PS   Claim 69; Page 233; 387pp; English.
XX
CC   The present invention relates to the treatment, prevention or
CC   amelioration of a disease or disorder associated with: aberrant B
CC   lymphocyte stimulator (BLyS), BLyS receptor expression or activity; cells
CC   of haematopoietic origin; or proliferative disease; and reducing,
CC   inhibiting or stimulating immunoglobulin production, B cell proliferation
CC   and graft rejection involving administration of BLyS binding polypeptide.
CC   The BLyS binding polypeptides are used in the treatment, prevention or
CC   amelioration of diseases such as immune system diseases, proliferative
CC   diseases, diseases of cells of hematopoietic origin, graft rejection,
CC   allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC   hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC   neurodegenerative diseases. The present sequence is a B lymphocyte
CC   stimulator protein binding peptide
XX
SQ   Sequence 7 AA;

  Query Match             89.5%;  Score 34;  DB 5;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CXPXTGC 7
              |||||||
Db          1 CXPXTGC 7


RESULT 9
ABG33862
ID   ABG33862 standard; peptide; 7 AA.
XX
AC   ABG33862;
XX
DT   15-JUL-2002  (first entry)
XX
DE   B Lymphocyte Stimulator (BLyS) binding peptide #436.
XX
KW   B Lymphocyte Stimulator protein; B Lymphocyte Stimulator binding peptide;
KW   BLyS; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid;
KW   synovial fluid; saliva; mucus.
XX
```

OS Synthetic.
XX
PN WO200216412-A2.
XX
PD 28-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-US025891.
XX
PR 18-AUG-2000; 2000US-0226489P.
XX
PA (DYAX-) DYAX CORP.
XX
PI Beltzer JP, Potter MD, Fleming TJ, Ladner RC;
XX
DR WPI; 2002-351647/38.
XX
PT New B-lymphocyte stimulator binding polypeptide useful in detecting or
PT isolating BLyS or BLyS-like polypeptide comprises a specified amino acid
PT sequence.
XX
PS Disclosure; Page 132; 269pp; English.
XX
CC The invention relates to a B Lymphocyte Stimulator (BLyS) binding
CC polypeptide. BLyS binding peptides bind BLyS or BLyS-like proteins
CC reversibly or irreversibly. The binding peptides are used in detection,
CC isolation and/or purification of BLyS in a solution such as water or a
CC buffer solution, as well as any fluid and/or cell obtained from an
CC individual biological fluid, body tissue, body cell, cell line, tissue
CC culture or other source containing BLyS or BLyS-like polypeptides. The
CC biological fluids include sera, plasma, lymph, blood, blood fraction,
CC urine, synovial fluid, spinal fluid, saliva and mucous. Sequences
CC ABG33406-33415, ABG33423-33575, ABG33588-33846, ABG33848-33850 and
CC ABG33852-33862 represent BLyS binding peptides of the invention
XX
SQ Sequence 7 AA;

Query Match 89.5%; Score 34; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXPXTGC 7
|||||||
Db 1 CXPXTGC 7

RESULT 10
ABJ00545
ID ABJ00545 standard; peptide; 13 AA.
XX
AC ABJ00545;
XX
DT 05-SEP-2002 (first entry)
XX
DE B lymphocyte stimulator protein binding protein consensus peptide #1.
XX
KW B lymphocyte stimulator protein binding protein; BLyS; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW antiasthmatic; antiallergic; thyromimetic; antianaemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Misc-difference 1
FT /label= Ala, Asn, Lys, Ser
FT Misc-difference 2
FT /label= Ala, Glu, Met, Ser, Val
FT Misc-difference 3
FT /label= Ala, Asn, Lys, Pro
FT Misc-difference 5
FT /label= Phe, Trp, Tyr
FT Misc-difference 7
FT /label= Pro, Tyr
FT Misc-difference 11
FT /label= Ala, Gln, His, Phe, Val
FT Misc-difference 12
FT /label= Asn, Gln, Gly, His, Ser, Val
FT Misc-difference 13
FT /label= Ala, Asn, Gly, Ile, Pro, Ser
XX
PN WO200216411-A2.
XX
PD 28-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-US025850.
XX
PR 18-AUG-2000; 2000US-0226700P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;
XX
DR WPI; 2002-499775/53.
XX
PT The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B Lymphocyte stimulator binding polypeptide.
XX
PS Claim 69; Page 230; 387pp; English.
XX
CC The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (BLyS), BLyS receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of BLyS binding polypeptide.
CC The BLyS binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a conserved region of
CC a B lymphocyte stimulator protein binding peptide
XX
SQ Sequence 13 AA;

Query Match 89.5%; Score 34; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXPXTGC 7
|||||||
Db 4 CXPXTGC 10

RESULT 11
ABG33861
ID ABG33861 standard; peptide; 13 AA.
XX
AC ABG33861;
XX
DT 15-JUL-2002 (first entry)
XX
DE B Lymphocyte Stimulator (BLyS) binding peptide #435.
XX
KW B Lymphocyte Stimulator protein; B Lymphocyte Stimulator binding peptide;
KW BLyS; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid;
KW synovial fluid; saliva; mucus.
XX
OS Synthetic.
XX
PN WO200216412-A2.

XX
PD 28-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-US025891.
XX
PR 18-AUG-2000; 2000US-0226489P.
XX
PA (DYAX-) DYAX CORP.
XX
PI Beltzer JP, Potter MD, Fleming TJ, Ladner RC;
XX
DR WPI; 2002-351647/38.
XX
PT New B-lymphocyte stimulator binding polypeptide useful in detecting or
PT isolating BLyS or BLyS-like polypeptide comprises a specified amino acid
PT sequence.
XX
PS Disclosure; Page 121; 269pp; English.
XX
CC The invention relates to a B Lymphocyte Stimulator (BLyS) binding
CC polypeptide. BLyS binding peptides bind BLyS or BLyS-like proteins
CC reversibly or irreversibly. The binding peptides are used in detection,
CC isolation and/or purification of BLyS in a solution such as water or a
CC buffer solution, as well as any fluid and/or cell obtained from an
CC individual biological fluid, body tissue, body cell, cell line, tissue
CC culture or other source containing BLyS or BLyS-like polypeptides. The
CC biological fluids include sera, plasma, lymph, blood, blood fraction,
CC urine, synovial fluid, spinal fluid, saliva and mucous. Sequences
CC ABG33406-33415, ABG33423-33575, ABG33588-33846, ABG33848-33850 and
CC ABG33852-33862 represent BLyS binding peptides of the invention
XX
SQ Sequence 13 AA;

Query Match 89.5%; Score 34; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXPXTGC 7
|||||||
Db 4 CXPXTGC 10

RESULT 12
AAU44932
ID AAU44932 standard; protein; 53 AA.
XX
AC AAU44932;
XX
DT 27-FEB-2002 (first entry)
XX
DE Propionibacterium acnes immunogenic protein #5828.
XX
KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX
OS Propionibacterium acnes.
XX
PN WO200181581-A2.
XX
PD 01-NOV-2001.
XX
PF 20-APR-2001; 2001WO-US012865.
XX
PR 21-APR-2000; 2000US-0199047P.
PR 02-JUN-2000; 2000US-0208841P.
PR 07-JUL-2000; 2000US-0216747P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
DR WPI; 2001-616774/71.
DR N-PSDB; AAS59524.
XX
PT Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris.
XX
PS Example 1; SEQ ID NO 6127; 1069pp; English.
XX
CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 53 AA;

Query Match 89.5%; Score 34; DB 4; Length 53;
Best Local Similarity 71.4%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CXPXTGC 7
| | |||
Db 33 CRPRTGC 39

RESULT 13
ABM41451
ID ABM41451 standard; protein; 53 AA.
XX
AC ABM41451;
XX
DT 20-OCT-2003 (first entry)
XX
DE Propionibacterium acnes predicted ORF-encoded polypeptide #6127.
XX
KW Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
KW immunostimulant; immune response; vaccine.
XX
OS Propionibacterium acnes.
XX
PN WO2003033515-A1.
XX
PD 24-APR-2003.
XX
PF 11-OCT-2002; 2002WO-US032727.
XX
PR 15-OCT-2001; 2001US-00978825.
XX
PA (CORI-) CORIXA CORP.
XX
PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
PI Barth B, Vallieve-Douglass J;
XX
DR WPI; 2003-381789/36.
DR N-PSDB; ACF64453.

XX
PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
PT or for stimulating an immune response specific for a P. acnes protein.
XX
PS Example 1; SEQ ID NO 6127; 1481pp; English.
XX
CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
CC encoding a Propionibacterium acnes protein. The invention also relates to
CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
CC immunogenic fragments of P. acnes polypeptides. The invention
CC additionally encompasses expression vectors and host cells comprising a
CC polynucleotide of the invention; antibodies against polypeptides of the
CC invention; fusion proteins comprising a polypeptide of the invention; a
CC method for stimulating an immune response specific for a P. acnes
CC polypeptide and an isolated T cell population comprising T cells prepared
CC via this method; a vaccine composition (comprising P. acnes polypeptides,
CC polynucleotides, antibodies, fusion proteins, T cell populations, or
CC antigen-presenting cells that express the polypeptide); a method and kit
CC for detecting or determining the presence or absence of P. acnes in a
CC patient; and a method for inhibiting the development of P. acnes in a
CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
CC proteins, T cell populations or antigen-presenting cells that express the
CC polypeptides are useful for diagnosing, preventing or treating acne
CC vulgaris, or for stimulating an immune response specific for a P. acnes
CC protein. The polynucleotides can also be used as probes or primers for
CC nucleic acid hybridisation. The vaccine composition is useful for the
CC stimulation of an immune response against P. acnes, or for treating acne,
CC and the kit is useful for performing a diagnostic assay. The present
CC sequence represents a polypeptide predicted to be encoded by an ORF (open
CC reading frame) contained within the P. acnes polynucleotides of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 53 AA;

Query Match 89.5%; Score 34; DB 6; Length 53;
Best Local Similarity 71.4%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CXPXTGC 7
| | |||
Db 33 CRPRTGC 39

RESULT 14
ADA54961
ID ADA54961 standard; protein; 113 AA.
XX
AC ADA54961;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human protein, SEQ ID 2529.
XX
KW Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
KW Gene Therapy; human; secretory protein; membrane proteins; cancer;
KW inflammatory disease; osteoporosis; neurological disease.
XX
OS Homo sapiens.
XX
PN EP1293569-A2.
XX
PD 19-MAR-2003.
XX
PF 21-MAR-2002; 2002EP-00006586.
XX
PR 14-SEP-2001; 2001JP-00328381.
PR 24-JAN-2002; 2002US-0350435P.
XX
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI; 2003-395539/38.
DR N-PSDB; ADA53322.
XX
PT New polynucleotides encoding full-length polypeptides, e.g. secretory
PT and/or membrane proteins, useful for developing medicines for diseases in
PT which the gene is involved, or as target molecules for gene therapy.
XX
PS Claim 14; SEQ ID NO 2529; 205pp; English.
XX
CC The present invention relates to novel human secretory or membrane
CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
CC ADA54071). The coding sequences are useful in the gene therapy of
CC diseases caused by abnormalities of the proteins, e.g. cancer,
CC inflammatory diseases, osteoporosis or neurological disease.
XX
SQ Sequence 113 AA;

Query Match 89.5%; Score 34; DB 6; Length 113;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CXPXTGC 7
| | |||
Db 103 CYPKTGC 109

RESULT 15
AAB42027
ID AAB42027 standard; protein; 138 AA.
XX
AC AAB42027;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human ORFX ORF1791 polypeptide sequence SEQ ID NO:3582.
XX
KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cholesterol ester storage; systemic lupus erythematosus; infection;
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW thrombosis; contraceptive.
XX
OS Homo sapiens.
XX
PN WO200058473-A2.
XX
PD 05-OCT-2000.
XX
PF 31-MAR-2000; 2000WO-US008621.
XX
PR 31-MAR-1999; 99US-0127607P.
PR 02-APR-1999; 99US-0127636P.
PR 05-APR-1999; 99US-0127728P.
PR 30-MAR-2000; 2000US-00540763.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX

DR WPI; 2000-602362/57.
DR N-PSDB; AAC76236.
XX
PT Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease.
XX
PS Claim 11; Page 2743; 5507pp; English.
XX
CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC sequences have activities such as: cytostatic; hepatotropic; vulnerary;
CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
CC anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
CC dermatological; immunosuppressive; antiinflammatory; antibacterial;
CC antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The
CC sequences can be used for determining the presence of or predisposition
CC to, or preventing or treating pathological conditions associated with an
CC ORFX-associated disorder. The nucleic acids can be used to express ORFX
CC proteins in gene therapy vectors. The proteins and nucleic acids may be
CC used to treat cancers, proliferative disorders, neurodegenerative
CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
CC storage, systemic lupus erythematosus, severe combined immunodeficiency
CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
CC cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
CC enhance coagulation; to inhibit thrombosis; and as a contraceptive
XX
SQ Sequence 138 AA;

Query Match 89.5%; Score 34; DB 3; Length 138;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 CXPXTGC 7
              | | |||
Db         15 CGPRTGC 21
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Search completed: January 12, 2005, 23:10:52
Job time : 79.1 secs